



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 148190

**TO: Phillip Gabel
Location: rem/3c70
Art Unit: 1644
Thursday, March 24, 2005**

Case Serial Number: 10/018245

**From: Alex Waclawiw
Location: Biotech-Chem Library
CM1-6A02
Phone: 308-4491**

Alexandra.waclawiw@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

148 190

mej

From: Gambel, Phillip
Sent: Saturday, March 19, 2005 9:43 AM
To: STIC-Biotech/ChemLib
Subject: 10 / 018,245 Fukuda

stic

RECEIVED
MAR 21 2005
STIC

please perform a Sequence and a Sequence Interference Search for

in Paper

10 / 018,245 Fukuda tnf-specific antibodies

SEQ ID NO: 1

SEQ ID NO: 2

SEQ ID NO: 3

SEQ ID NO: 4

SEQ ID NO: 5

SEQ ID NO: 6

thanx

phillip gambel
art unit 1644
272-0844

1644 mailbox 3c70

*****Point of Contact:
STAFF USE ONLY Alexandra Wacławiw
Technical Info. Specialist
Searcher: CM1 6A02 Tel: 308-4491
Searcher Phone: 2-
Date Searcher Picked up: _____
Date Completed: _____ 10
Searcher Prep/Rev. Time: _____
Online Time: _____ 12

Type of Search
NA#: _____ AA#: 6
Interference: ☒ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): CompuLink

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 75.9375 Seconds
(without alignments)
50.931 Million cell updates/sec

Title: US-10-018-245A-1
Perfect score: 59
Sequence: 1 GYFTMYGNM 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	10	2	AAW70611
2	59	100.0	10	5	AAAG80311
3	59	100.0	10	5	ABP61180
4	59	100.0	10	8	ADR89785
5	59	100.0	67	7	ADH62639
6	59	100.0	70	7	ADH62638
7	59	100.0	70	7	ADH62637
8	59	100.0	92	2	AAW24529
9	59	100.0	92	5	AAU80997
10	59	100.0	112	2	AAW24521
11	59	100.0	112	5	AAU80980
12	59	100.0	115	4	AAAB84740
13	59	100.0	116	4	AAAB84739
14	59	100.0	116	5	AAE27830
15	59	100.0	116	5	AAE27839
16	59	100.0	116	5	AAE27837
17	59	100.0	116	5	AAE27825
18	59	100.0	116	5	AAE27826
19	59	100.0	116	5	AAE27828
20	59	100.0	116	5	AAE27832
21	59	100.0	116	5	AAE27834
22	59	100.0	116	5	ADG67541
23	59	100.0	116	5	ADG67537
24	59	100.0	116	5	ADG67543
25	59	100.0	116	5	ADG67531

26	59	100.0	116	5	ADG67533	ADG67533 KS antibo
27	59	100.0	116	5	ADG67539	ADG67539 KS antibo
28	59	100.0	116	5	ADG67529	ADG67529 KS antibo
29	59	100.0	116	5	ADG67535	ADG67535 KS antibo
30	59	100.0	116	6	AAE33431	AAE33431 Murine KS
31	59	100.0	116	6	AAE33433	AAE33433 Murine KS
32	59	100.0	116	6	AAE33418	AAE33418 Heavy cha
33	59	100.0	116	6	AAE33434	AAE33434 Murine KS
34	59	100.0	116	6	AAE33435	AAE33435 Murine KS
35	59	100.0	116	6	AAE33414	AAE33414 Murine KS
36	59	100.0	116	6	AAE33432	AAE33432 Murine KS
37	59	100.0	116	6	AAE33438	AAE33438 Murine KS
38	59	100.0	116	6	AAE33429	AAE33429 Murine KS
39	59	100.0	116	6	AAE33430	AAE33430 Murine KS
40	59	100.0	116	6	AAE33437	AAE33437 Murine KS
41	59	100.0	116	6	AAE33416	AAE33416 EPCAM ant
42	59	100.0	116	6	AAE33436	AAE33436 Murine KS
43	59	100.0	116	6	AAO30908	AAO30908 hu-KS ant
44	59	100.0	116	6	AAO30911	AAO30911 di-KS ant
45	59	100.0	117	2	AAE28750	AAE28750 Heavy cha
46	59	100.0	117	5	AAE28752	AAE28752 Heavy cha
47	59	100.0	117	5	AAE28752	AAE28752 Heavy cha
48	59	100.0	117	6	AAE33439	AAE33439 Murine KS
49	59	100.0	117	8	ADG34377	ADG34377 Humanised
50	59	100.0	117	8	ADG34374	ADG34374 Humanised
51	59	100.0	117	8	ADG34375	ADG34375 Humanised
52	59	100.0	117	8	ADG34376	ADG34376 Humanised
53	59	100.0	117	8	ADG34376	ADG34376 Humanised
54	59	100.0	118	2	AAE28496	AAE28496 Human ECL
55	59	100.0	118	2	AAE28412	AAE28412 Heavy cha
56	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
57	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
58	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
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62	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
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68	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
69	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
70	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
71	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
72	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
73	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
74	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
75	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
76	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
77	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
78	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
79	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
80	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
81	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
82	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
83	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
84	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
85	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
86	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
87	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
88	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
89	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
90	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
91	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
92	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
93	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
94	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
95	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
96	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
97	59	100.0	118	2	AAE28414	AAE28414 Heavy cha
98	59	100.0	118	2	AAE28414	AAE28414 Heavy cha

99 59 100.0 123 2 AAW86807
100 59 100.0 123 2 AAW70617

AAW86807 Variable
AAW70617 Anti-VEGF

ALIGNMENTS

RESULT 1
ID AAW70611 standard; peptide; 10 AA.

XX AAW70611;

XX 27-JAN-1999 (first entry)

DE Anti-VEGF antibody heavy chain hypervariable region CDRH1.

XX Heavy chain hypervariable region; murine; humanised antibody;
XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
XX VEGF-induced angiogenesis; tumour; retinal disorder;
XX age-related macular degeneration; diabetic retinopathy;
XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX Synthetic.

OS Mus sp.

XX WO9845331-A2.

XX 15-OCT-1998.

XX 03-APR-1998; 98WO-US006604.

XX 07-APR-1997; 97US-00833504.

PR 06-AUG-1997; 97US-00908469.

XX (GETH) GENENTECH INC.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM,

DR WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours; retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.

XX Claim 8; Page 79; 100pp; English.

XX The present sequence represents a heavy chain hypervariable region of the
CC murine anti-vascular endothelial growth factor (anti-VEGF) antibody. The
CC sequence is used to construct the humanised anti-VEGF antibody of the
CC invention. The humanised antibodies are used to inhibit VEGF-induced
CC angiogenesis, particularly for treating or preventing tumours (of any
CC type) and retinal disorders (e.g. age-related macular degeneration or
CC diabetic retinopathy). They can also be used to treat other conditions
CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
CC atherosclerosis, Grave's disease, etc

XX Sequence 10 AA;

Query Match 100.0%; Score 59; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTNYGMN 10
Db 1 GYFTNYGMN 10

RESULT 2
ID AAG80311 standard; peptide; 10 AA.
XX AAG80311;
AC AAG80311;

XX 18-FEB-2002 (first entry)
DT Anti-human TNF-alpha CDR-H1 peptide.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
XX heavy chain; light chain; complementarity determining region; vasotropic;
XX antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
XX rheumatoid arthritis; malaria; multiple sclerosis.

OS Homo sapiens.

XX WO200179298-A1.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-JP033308.

XX 19-APR-2000; 2000JP-00117394.

XX (SUNR) SUNTORY LTD.

XX Fukuda Y, Nagahira K, Nakanishi T;

XX WPI; 2002-066345/09.

XX Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX Claim 1a; Page 25; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotropic, antiarthritic, neuroprotective and
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
CC vivo. The antibodies are used for producing chimeric and humanised
CC antibodies that may be used for the treatment and prevention of TNF-alpha
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC humans. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) heavy chain CDR1 designated CDR-H1

XX Sequence 10 AA;

Query Match 100.0%; Score 59; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTNYGMN 10
Db 1 GYFTNYGMN 10

RESULT 3
ID ABP61180

XX ABP61180 standard; peptide; 10 AA.

XX AC ABP61180;

XX 20-SEP-2002 (first entry)

XX Humanised anti-VEGF antibody heavy chain variable domain, CDRH1.

XX Cytostratic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
XX vascular endothelial growth factor; angiogenesis inhibitor; tumour;
XX retinal disorder; intraocular neovascular disorder; heavy chain;
XX variable domain; CDRH1.

OS Homo sapiens.
OS Mus sp.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:57:11 ; Search time 20.1562 Seconds
(without alignments)
37.035 Million cell updates/sec

Title: US-10-018-245A-1
Perfect score: 59
Sequence: 1 GYFTNYGMW 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents_Aa:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.dep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.dep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.dep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.dep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.dep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.dep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	92	3	US-08-783-853A-84 Sequence 84, App1
2	59	100.0	92	3	US-09-344-050-84 Sequence 20, App1
3	59	100.0	112	3	US-08-783-853A-20 Sequence 20, App1
4	59	100.0	112	3	US-09-344-050-20 Sequence 20, App1
5	59	100.0	118	1	US-08-425-336-124 Sequence 124, App
6	59	100.0	118	1	US-08-425-336-126 Sequence 126, App
7	59	100.0	118	1	US-08-488-113B-124 Sequence 124, App
8	59	100.0	118	1	US-08-488-113B-126 Sequence 126, App
9	59	100.0	118	1	US-08-477-484B-124 Sequence 124, App
10	59	100.0	118	1	US-08-477-484B-126 Sequence 126, App
11	59	100.0	118	1	US-08-107-669D-28 Sequence 28, App1
12	59	100.0	118	1	US-08-107-669D-29 Sequence 29, App1
13	59	100.0	118	1	US-08-107-669D-66 Sequence 66, App1
14	59	100.0	118	1	US-08-107-669D-67 Sequence 67, App1
15	59	100.0	118	1	US-08-477-788A-28 Sequence 28, App1
16	59	100.0	118	1	US-08-477-788A-29 Sequence 29, App1
17	59	100.0	118	1	US-08-472-788A-88 Sequence 88, App1
18	59	100.0	118	1	US-08-472-788A-89 Sequence 89, App1
19	59	100.0	118	1	US-08-477-531B-28 Sequence 28, App1
20	59	100.0	118	2	US-08-477-531B-29 Sequence 29, App1
21	59	100.0	118	2	US-08-477-531B-66 Sequence 66, App1
22	59	100.0	118	2	US-08-477-531B-67 Sequence 67, App1
23	59	100.0	118	2	US-08-646-360-124 Sequence 124, App
24	59	100.0	118	2	US-08-646-360-126 Sequence 126, App
25	59	100.0	118	2	US-08-082-842A-28 Sequence 28, App1
26	59	100.0	118	2	US-08-082-842A-29 Sequence 29, App1
27	59	100.0	118	2	US-08-082-842A-88 Sequence 88, App1

28	59	100.0	118	2	US-08-082-842A-89 Sequence 89, App1
29	59	100.0	118	3	US-08-839-765-124 Sequence 124, App
30	59	100.0	118	3	US-08-839-765-126 Sequence 126, App
31	59	100.0	118	3	US-09-136-389-124 Sequence 124, App
32	59	100.0	118	3	US-09-136-389-126 Sequence 126, App
33	59	100.0	118	3	US-09-610-838-124 Sequence 124, App
34	59	100.0	118	3	US-09-610-838-126 Sequence 126, App
35	59	100.0	118	4	US-09-440-781-96 Sequence 96, App1
36	59	100.0	118	4	US-09-711-485-124 Sequence 124, App
37	59	100.0	118	4	US-09-711-485-126 Sequence 126, App
38	59	100.0	119	3	US-08-933-983-78 Sequence 78, App1
39	59	100.0	119	3	US-08-933-983-80 Sequence 80, App1
40	59	100.0	120	4	US-09-232-290-48 Sequence 48, App1
41	59	100.0	121	3	US-08-783-853A-7 Sequence 7, App1
42	59	100.0	121	3	US-08-783-853A-31 Sequence 31, App1
43	59	100.0	121	3	US-08-783-853A-52 Sequence 52, App1
44	59	100.0	121	3	US-08-783-853A-111 Sequence 111, App
45	59	100.0	121	3	US-09-344-050-7 Sequence 7, App1
46	59	100.0	121	3	US-09-344-050-31 Sequence 31, App1
47	59	100.0	121	3	US-09-344-050-52 Sequence 52, App1
48	59	100.0	121	3	US-09-344-050-111 Sequence 111, App
49	59	100.0	121	4	US-09-440-781-98 Sequence 98, App1
50	59	100.0	123	3	US-08-783-853A-109 Sequence 109, App
51	59	100.0	123	3	US-09-344-050-109 Sequence 109, App
52	59	100.0	138	3	US-08-933-983-11 Sequence 11, App1
53	59	100.0	138	3	US-08-933-983-15 Sequence 15, App1
54	59	100.0	139	3	US-08-933-983-19 Sequence 19, App1
55	59	100.0	139	3	US-08-933-983-21 Sequence 21, App1
56	59	100.0	140	3	US-08-783-853A-89 Sequence 89, App1
57	59	100.0	140	3	US-09-344-050-89 Sequence 89, App1
58	59	100.0	240	1	US-08-488-113B-147 Sequence 147, App
59	59	100.0	240	1	US-08-488-113B-148 Sequence 148, App
60	59	100.0	240	1	US-08-477-484B-147 Sequence 147, App
61	59	100.0	240	1	US-08-477-484B-148 Sequence 148, App
62	59	100.0	240	2	US-08-646-360-147 Sequence 147, App
63	59	100.0	240	2	US-08-646-360-148 Sequence 148, App
64	59	100.0	240	3	US-08-839-765-147 Sequence 147, App
65	59	100.0	240	3	US-08-839-765-148 Sequence 148, App
66	59	100.0	240	3	US-09-136-389-147 Sequence 147, App
67	59	100.0	240	3	US-09-136-389-148 Sequence 148, App
68	59	100.0	240	3	US-09-610-838-147 Sequence 147, App
69	59	100.0	240	3	US-09-610-838-148 Sequence 148, App
70	59	100.0	240	4	US-09-711-485-147 Sequence 147, App
71	59	100.0	240	4	US-09-711-485-148 Sequence 148, App
72	59	100.0	250	1	US-08-133-804-2 Sequence 2, App1
73	59	100.0	250	1	US-08-461-184-8 Sequence 8, App1
74	59	100.0	250	1	US-08-463-675-8 Sequence 8, App1
75	59	100.0	250	1	US-08-464-589-8 Sequence 8, App1
76	59	100.0	250	1	US-08-461-838-2 Sequence 2, App1
77	59	100.0	250	2	US-08-461-838-2 Sequence 2, App1
78	59	100.0	252	2	US-08-279-772A-6 Sequence 6, App1
79	59	100.0	252	3	US-08-902-486-9 Sequence 9, App1
80	59	100.0	365	3	US-08-875-811-53 Sequence 53, App1
81	59	100.0	366	3	US-08-875-811-55 Sequence 55, App1
82	59	100.0	421	4	US-10-011-125A-2 Sequence 2, App1
83	59	100.0	622	2	US-08-356-786-16 Sequence 16, App1
84	59	93.2	622	3	US-08-569-147-76 Sequence 76, App1
85	55	93.2	140	3	US-08-569-147-82 Sequence 82, App1
86	55	93.2	140	4	US-09-318-786-35 Sequence 35, App1
87	54	91.5	115	3	US-08-483-749A-24 Sequence 24, App1
88	54	91.5	230	3	US-09-485-737B-102 Sequence 102, App
89	54	91.5	230	4	US-10-071-485-102 Sequence 102, App
90	54	91.5	235	4	US-09-485-737B-93 Sequence 93, App1
91	54	91.5	235	4	US-10-071-485-93 Sequence 93, App1
92	54	91.5	240	3	US-09-485-737B-91 Sequence 91, App1
93	54	91.5	240	4	US-10-071-485-91 Sequence 91, App1
94	54	91.5	243	1	US-08-133-804-6 Sequence 6, App1
95	54	91.5	243	1	US-08-461-838-6 Sequence 6, App1
96	54	91.5	243	2	US-08-461-838-6 Sequence 6, App1
97	54	91.5	243	2	US-08-356-786-6 Sequence 6, App1
98	54	91.5	267	3	US-09-485-737B-2 Sequence 2, App1
99	54	91.5	267	4	US-10-071-485-2 Sequence 2, App1
100	54	91.5	468	3	US-09-485-737B-67 Sequence 67, App1

ALIGNMENTS

RESULT 1
US-08-783-853A-84
Sequence 84, Application US/08783853A
Patent No. 6005091
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padian, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-783-853A-84

Query Match 100.0%; Score 59; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTNYGMN 10
|||||
Db 3 GYFTNYGMN 12

RESULT 2
US-09-344-050-84
Sequence 84, Application US/09344050

Patent No. 5391299
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padian, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-09-344-050-84

Query Match 100.0%; Score 59; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTNYGMN 10
|||||
Db 3 GYFTNYGMN 12

RESULT 3
US-08-783-853A-20
Sequence 20, Application US/08783853A
Patent No. 6005091
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padian, Eduardo

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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:56:15 ; Search time 57.6562 Seconds
(without alignments)
57.427 Million cell updates/sec

Title: US-10-018-245A-1
Perfect score: 59
Sequence: 1 GYFTNXXNM 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 31100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*
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16: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	59	100.0	10	14	US-10-234-671-1
3	59	100.0	10	16	US-10-018-245A-1
4	59	100.0	10	16	US-10-723-434-112
5	59	100.0	10	16	US-10-723-434-116
6	59	100.0	10	16	US-10-723-434-116
7	59	100.0	67	14	US-10-243-130-19
8	59	100.0	70	14	US-10-243-130-17
9	59	100.0	70	14	US-10-243-130-18
10	59	100.0	70	14	US-10-243-130-18
11	59	100.0	70	17	US-10-901-650-17
12	59	100.0	70	17	US-10-901-650-18
13	59	100.0	92	9	US-09-965-099-84
			92	13	US-10-051-852-84

14	59	100.0	92	15	US-10-430-176-84	Sequence 84, Appl
15	59	100.0	112	9	US-09-965-099-20	Sequence 20, Appl
16	59	100.0	112	13	US-10-051-852-20	Sequence 20, Appl
17	59	100.0	112	15	US-10-430-176-20	Sequence 20, Appl
18	59	100.0	116	9	US-09-971-543-9	Sequence 9, Appl
19	59	100.0	116	9	US-09-971-543-9	Sequence 9, Appl
20	59	100.0	116	9	US-09-971-543-10	Sequence 10, Appl
21	59	100.0	116	14	US-10-138-727A-2	Sequence 2, Appl
22	59	100.0	116	14	US-10-138-727A-4	Sequence 4, Appl
23	59	100.0	116	14	US-10-138-727A-6	Sequence 6, Appl
24	59	100.0	116	14	US-10-138-727A-17	Sequence 17, Appl
25	59	100.0	116	14	US-10-138-727A-19	Sequence 19, Appl
26	59	100.0	116	14	US-10-138-727A-19	Sequence 19, Appl
27	59	100.0	116	14	US-10-138-727A-20	Sequence 20, Appl
28	59	100.0	116	14	US-10-138-727A-21	Sequence 21, Appl
29	59	100.0	116	14	US-10-138-727A-22	Sequence 22, Appl
30	59	100.0	116	14	US-10-138-727A-23	Sequence 23, Appl
31	59	100.0	116	14	US-10-138-727A-24	Sequence 24, Appl
32	59	100.0	116	14	US-10-138-727A-25	Sequence 25, Appl
33	59	100.0	116	14	US-10-138-727A-26	Sequence 26, Appl
34	59	100.0	116	14	US-10-310-719-30	Sequence 30, Appl
35	59	100.0	116	14	US-10-310-719-33	Sequence 33, Appl
36	59	100.0	116	15	US-10-468-370-658	Sequence 658, Appl
37	59	100.0	116	15	US-10-468-370-660	Sequence 660, Appl
38	59	100.0	116	15	US-10-468-370-662	Sequence 662, Appl
39	59	100.0	116	15	US-10-468-370-664	Sequence 664, Appl
40	59	100.0	116	15	US-10-468-370-666	Sequence 666, Appl
41	59	100.0	116	15	US-10-468-370-668	Sequence 668, Appl
42	59	100.0	116	15	US-10-468-370-670	Sequence 670, Appl
43	59	100.0	116	15	US-10-468-370-672	Sequence 672, Appl
44	59	100.0	116	16	US-10-468-496-2021	Sequence 2021, Appl
45	59	100.0	116	16	US-10-468-496-2023	Sequence 2023, Appl
46	59	100.0	116	16	US-10-468-496-2025	Sequence 2025, Appl
47	59	100.0	116	16	US-10-468-496-2027	Sequence 2027, Appl
48	59	100.0	116	16	US-10-468-496-2029	Sequence 2029, Appl
49	59	100.0	116	16	US-10-468-496-2031	Sequence 2031, Appl
50	59	100.0	116	16	US-10-468-496-2033	Sequence 2033, Appl
51	59	100.0	116	16	US-10-468-496-2035	Sequence 2035, Appl
52	59	100.0	117	14	US-10-422-049-15	Sequence 15, Appl
53	59	100.0	117	14	US-10-422-049-16	Sequence 16, Appl
54	59	100.0	117	14	US-10-422-049-16	Sequence 16, Appl
55	59	100.0	118	9	US-09-056-160B-104	Sequence 104, Appl
56	59	100.0	118	14	US-10-234-671-102	Sequence 102, Appl
57	59	100.0	118	14	US-10-234-671-104	Sequence 104, Appl
58	59	100.0	118	14	US-10-268-883-9	Sequence 9, Appl
59	59	100.0	118	14	US-10-127-890-124	Sequence 124, Appl
60	59	100.0	118	14	US-10-127-890-126	Sequence 126, Appl
61	59	100.0	118	14	US-10-234-671-7	Sequence 7, Appl
62	59	100.0	118	14	US-10-234-671-102	Sequence 102, Appl
63	59	100.0	118	14	US-10-234-671-104	Sequence 104, Appl
64	59	100.0	118	14	US-10-234-671-106	Sequence 106, Appl
65	59	100.0	118	14	US-10-422-049-15	Sequence 15, Appl
66	59	100.0	118	14	US-10-422-049-19	Sequence 19, Appl
67	59	100.0	118	15	US-10-340-189-28	Sequence 28, Appl
68	59	100.0	118	15	US-10-340-189-29	Sequence 29, Appl
69	59	100.0	118	15	US-10-340-189-88	Sequence 88, Appl
70	59	100.0	118	15	US-10-340-189-88	Sequence 88, Appl
71	59	100.0	118	15	US-10-325-696-28	Sequence 28, Appl
72	59	100.0	118	15	US-10-325-696-29	Sequence 29, Appl
73	59	100.0	118	15	US-10-325-696-66	Sequence 66, Appl
74	59	100.0	118	15	US-10-325-696-67	Sequence 67, Appl
75	59	100.0	118	15	US-10-624-671-96	Sequence 96, Appl
76	59	100.0	118	17	US-10-683-043-9	Sequence 9, Appl
77	59	100.0	118	17	US-10-683-043-14	Sequence 14, Appl
78	59	100.0	118	17	US-10-717-243-124	Sequence 124, Appl
79	59	100.0	118	17	US-10-717-243-126	Sequence 126, Appl
80	59	100.0	119	8	US-08-934-000-78	Sequence 78, Appl
81	59	100.0	119	8	US-08-934-000-80	Sequence 80, Appl
82	59	100.0	119	10	US-09-977-283A-78	Sequence 78, Appl
83	59	100.0	119	10	US-09-977-283A-80	Sequence 80, Appl
84	59	100.0	120	15	US-10-377-121-4	Sequence 4, Appl
85	59	100.0	120	15	US-10-377-121-9	Sequence 9, Appl
86	59	100.0	121	9	US-09-965-099-7	Sequence 7, Appl

87 59 100.0 121 9 US-09-965-099-31 Sequence 31, Appl
88 59 100.0 121 9 US-09-965-099-52 Sequence 52, Appl
89 59 100.0 121 9 US-09-965-099-111 Sequence 111, Appl
90 59 100.0 121 13 US-10-051-852-7 Sequence 7, Appl
91 59 100.0 121 13 US-10-051-852-31 Sequence 31, Appl
92 59 100.0 121 13 US-10-051-852-52 Sequence 52, Appl
93 59 100.0 121 13 US-10-051-852-111 Sequence 111, Appl
94 59 100.0 121 15 US-10-430-176-7 Sequence 7, Appl
95 59 100.0 121 15 US-10-430-176-31 Sequence 31, Appl
96 59 100.0 121 15 US-10-430-176-52 Sequence 52, Appl
97 59 100.0 121 15 US-10-430-176-111 Sequence 111, Appl
98 59 100.0 121 15 US-10-377-121-14 Sequence 14, Appl
99 59 100.0 121 15 US-10-624-153-98 Sequence 98, Appl
100 59 100.0 121 17 US-10-683-043-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-056-160B-1
Sequence 1, Application US/09056160B
Patent No. US20020032315A1

GENERAL INFORMATION:

APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-1

Query Match 100.0%; Score 59; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGMN 10
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Db 1 GYFTNYGMN 10

RESULT 2
US-10-234-671-1
Sequence 1, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-Apr-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-Apr-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-234-671-1

Query Match 100.0%; Score 59; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGMN 10
|||
Db 1 GYFTNYGMN 10

RESULT 3
US-10-018-245A-1
Sequence 1, Application US/10018245A
Publication No. US20040115196A1
GENERAL INFORMATION:
APPLICANT: FUKUDA, Yoshiaki
APPLICANT: NAKAMISHI, Toshihiro
APPLICANT: NAGAHIRA, Kazuhiro
TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
FILE REFERENCE: 46224
CURRENT APPLICATION NUMBER: US/10/018,245A
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: JP 117394/2000

Query Match 100.0%; Score 59; DB 14; Length 10;
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGMN 10
|||
Db 1 GYFTNYGMN 10

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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 14.0625 Seconds
(without alignments)
68.421 Million cell updates/sec

Title: US-10-018-245A-1
Perfect score: 59
Sequence: 1 GYTFNTYGMN 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: PIR.79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	59	100.0	99	2 S26326	Ig heavy chain V r
3	59	100.0	101	2 D24672	Ig heavy chain V r
4	59	100.0	105	2 S24764	Ig heavy chain V r
5	59	100.0	105	2 S24765	Ig heavy chain V r
6	59	100.0	109	2 S26335	Ig heavy chain V r
7	59	100.0	115	2 S19968	Ig heavy chain V r
8	59	100.0	115	2 S19965	Ig heavy chain V r
9	59	100.0	118	2 S19967	Ig heavy chain V r
10	59	100.0	119	2 A53285	Ig heavy chain V a
11	59	100.0	120	2 B42848	L6 mab heavy chain
12	59	100.0	124	2 PH1404	Ig heavy chain V r
13	59	100.0	146	4 S33905	Ig heavy chain pre
14	55	93.2	140	2 A36194	Ig heavy chain V r
15	54	91.5	113	2 B36259	Ig heavy chain V r
16	54	91.5	119	2 PH1521	Ig heavy chain V r
17	54	91.5	119	2 PH1519	Ig heavy chain V r
18	54	91.5	136	2 S35759	Ig heavy chain V r
19	54	91.5	140	2 PH1489	BHP9D10 protein -
20	53	89.8	119	2 PH1516	Ig heavy chain V r
21	51	86.4	140	2 PH1488	Ig heavy chain V r
22	51	86.4	107	2 PH0987	Ig heavy chain V r
23	51	86.4	120	2 S12953	Ig heavy chain V r
24	50	84.7	76	2 B28572	Ig heavy chain V r
25	50	84.7	98	2 B24754	Ig heavy chain V r
26	50	84.7	98	2 A28572	Ig heavy chain V r
27	50	84.7	102	2 PH1491	Ig heavy chain V r
28	50	84.7	102	2 PH1490	Ig heavy chain V r
29	50	84.7	110	2 A32189	Ig heavy chain V r

30	50	84.7	114	2 PH1523	Ig heavy chain V r
31	50	84.7	114	2 PH1522	Ig heavy chain V r
32	50	84.7	118	2 S38565	Ig heavy chain V r
33	50	84.7	118	2 A24754	Ig heavy chain V r
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35	50	84.7	119	2 PH1505	Ig heavy chain V r
36	50	84.7	119	2 PH1518	Ig heavy chain V r
37	50	84.7	119	2 PH1517	Ig heavy chain V r
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42	50	84.7	119	2 PH1520	Ig heavy chain V r
43	50	84.7	121	2 A21854	Ig heavy chain V r
44	50	84.7	121	2 A26405	Ig heavy chain V r
45	50	84.7	123	2 G48677	Ig heavy chain V-D
46	50	84.7	123	2 F48677	Ig heavy chain V-D
47	50	84.7	123	2 E48677	Ig heavy chain V-D
48	50	84.7	134	2 S21916	Ig heavy chain V r
49	50	84.7	135	2 PH1494	Ig heavy chain V r
50	50	84.7	135	2 PH1492	Ig heavy chain V r
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52	50	84.7	140	2 PH1483	Ig heavy chain V r
53	50	84.7	140	2 PH1482	Ig heavy chain V r
54	49	83.1	98	2 S46460	Ig heavy chain V r
55	49	83.1	119	2 H45722	anti-glycoprotein
56	49	83.1	135	2 PH1493	Ig heavy chain V r
57	48	81.4	98	2 A49051	Ig heavy chain V7
58	48	81.4	105	2 S24763	Ig heavy chain V r
59	48	81.4	111	2 PH0988	Ig heavy chain V r
60	48	81.4	114	2 C32967	Ig heavy chain V r
61	48	81.4	116	2 S31667	Ig heavy chain V r
62	48	81.4	117	2 S31854	Ig heavy chain V r
63	48	81.4	117	2 S32190	Ig heavy chain V r
64	48	81.4	131	2 S26792	Ig heavy chain V r
65	48	81.4	142	2 S19245	Ig heavy chain pre
66	47	79.7	102	2 S42176	Ig gamma chain V r
67	47	79.7	102	2 C32530	Ig heavy chain V r
68	46	78.0	91	2 PH1004	Ig heavy chain V r
69	46	78.0	96	2 S17614	Ig heavy chain V r
70	46	78.0	96	2 S17613	Ig heavy chain V r
71	46	78.0	97	2 PH1155	Ig heavy chain V r
72	46	78.0	98	2 PH1106	Ig heavy chain V r
73	46	78.0	98	2 PH1144	Ig heavy chain V r
74	46	78.0	98	2 PH1151	Ig heavy chain V r
75	46	78.0	101	2 H37262	Ig heavy chain V r
76	46	78.0	103	2 PH0986	Ig heavy chain V r
77	46	78.0	106	2 S26318	Ig heavy chain V r
78	46	78.0	109	2 S26318	Ig heavy chain V r
79	46	78.0	110	2 S26317	Ig heavy chain V r
80	46	78.0	117	1 HYMSG39	Ig heavy chain pre
81	46	78.0	117	2 G45722	anti-glycoprotein
82	46	78.0	118	2 C30560	Ig heavy chain V r
83	46	78.0	119	2 B32530	Ig heavy chain V r
84	46	78.0	119	2 PH0089	Ig heavy chain V r
85	46	78.0	120	2 A54256	Ig heavy chain V r
86	46	78.0	121	1 G1HURL	Ig heavy chain V-I
87	46	78.0	136	2 PH0208	Ig heavy chain pre
88	46	78.0	140	2 PH1484	Ig heavy chain V r
89	46	78.0	140	2 S70442	Ig heavy chain pre
90	45	76.3	94	2 G32513	Ig heavy chain V r
91	45	76.3	96	2 D25155	Ig heavy chain V r
92	45	76.3	98	2 S26913	Ig heavy chain V r
93	45	76.3	98	2 S26919	Ig heavy chain V r
94	45	76.3	98	2 PH1160	Ig heavy chain V r
95	45	76.3	101	2 S42183	Ig gamma chain V r
96	45	76.3	109	2 PH0973	Ig heavy chain V r
97	45	76.3	111	2 S21925	Ig heavy chain V r
98	45	76.3	112	2 S09957	Ig heavy chain V-D
99	45	76.3	113	2 PH0974	Ig heavy chain V r
100	45	76.3	118	1 MHMS38	Ig heavy chain V r

ALIGNMENTS

RESULT 1

C24672

Ig heavy chain V region (VMU-1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C/Accession: C24672

R/Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A/Reference number: A91022; MUID:86055722; PMID:2998759

A/Accession: C24672

A/Molecule type: DNA

A/Residues: 1-93 <MIN>

A/Cross-references: GB:X03300; NID:G52375; PIDN:CAA27039.1; PID:G773221

A/Note: this sequence was determined from the differentiated gene

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 59; DB 2; Length 93;

Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGMN 10

Db 7 GYFTNYGMN 16

RESULT 2

S26326

Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998

C/Accession: S26326

R/Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a protein

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26326

A/Molecule type: mRNA

A/Residues: 1-99 <STA>

A/Cross-references: EMBL:X59174

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 59; DB 2; Length 99;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGMN 10

Db 6 GYFTNYGMN 15

RESULT 3

D24672

Ig heavy chain V region (VGMW-8) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C/Accession: D24672

R/Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A/Reference number: A91022; MUID:86055722; PMID:2998759

A/Accession: D24672

A/Molecule type: DNA

A/Residues: 1-101 <WIN>

A/Cross-references: GB:X03301; NID:G51757; PIDN:CAA27040.1; PID:G773215

A/Note: this sequence was determined from the differentiated gene

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 59; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGMN 10

Db 7 GYFTNYGMN 16

RESULT 4

S24764

Ig heavy chain V region (subgroup XI) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999

C/Accession: S24764; S24772; S24777

R/Klares, S.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24763

A/Accession: S24764

A/Molecule type: DNA

A/Residues: 1-105 <KLA>

A/Cross-references: EMBL:Z14999

A/Accession: S24772

A/Molecule type: DNA

A/Residues: 1-105 <KLM>

A/Cross-references: EMBL:Z15011

R/Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24776

A/Accession: S24777

A/Molecule type: DNA

A/Residues: 1-105 <THO>

A/Cross-references: EMBL:Z15020; NID:G52616; PIDN:CAA78739.1; PID:G52617

C/Genetics:

A/Inserts: 9/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 59; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 0.002;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGMN 10

Db 38 GYFTNYGMN 47

RESULT 5

S24765

Ig heavy chain V region (subgroup XI) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999

C/Accession: S24765; S24773; S24778

R/Klares, S.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24763

A/Accession: S24765

A/Molecule type: DNA

A/Residues: 1-105 <KLA>

A/Cross-references: EMBL:Z15001

A/Accession: S24773

A/Molecule type: DNA

A/Residues: 1-105 <KLM>

A/Cross-references: EMBL:Z15013

R/Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24776

A/Accession: S24778

A/Molecule type: DNA

A/Residues: 1-105 <THO>

A/Cross-references: EMBL:Z15022; NID:G52619; PIDN:CAA78741.1; PID:G52620

C/Genetics:

A/Inserts: 9/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 65.9375 Seconds
(without alignments)
77.661 Million cell updates/sec

Title: US-10-018-245A-1
Perfect score: 59
Sequence: 1 GYFTNYGMN 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

1: uniprot_03:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	91.5	241	2	Q921A6
2	50	84.7	120	1	Q921A6 mus musculus
3	50	84.7	140	1	Q921A6 mus musculus
4	49	83.1	125	2	Q921A6 mus musculus
5	46	78.0	117	1	Q921A6 mus musculus
6	46	78.0	121	1	Q921A6 mus musculus
7	46	78.0	159	2	Q921A6 mus musculus
8	46	78.0	481	2	Q921A6 mus musculus
9	46	78.0	485	2	Q921A6 mus musculus
10	45	76.3	118	1	Q921A6 mus musculus
11	45	76.3	140	2	Q921A6 mus musculus
12	44	74.6	119	2	Q921A6 mus musculus
13	44	74.6	463	2	Q921A6 mus musculus
14	43	72.9	102	2	Q921A6 mus musculus
15	43	72.9	111	1	Q921A6 mus musculus
16	43	72.9	113	1	Q921A6 mus musculus
17	43	72.9	113	1	Q921A6 mus musculus
18	43	72.9	113	1	Q921A6 mus musculus
19	43	72.9	113	1	Q921A6 mus musculus
20	43	72.9	113	1	Q921A6 mus musculus
21	43	72.9	113	1	Q921A6 mus musculus
22	43	72.9	113	1	Q921A6 mus musculus
23	43	72.9	113	1	Q921A6 mus musculus
24	43	72.9	113	1	Q921A6 mus musculus
25	43	72.9	117	1	Q921A6 mus musculus
26	43	72.9	120	2	Q921A6 mus musculus
27	43	72.9	123	2	Q921A6 mus musculus
28	43	72.9	136	1	Q921A6 mus musculus
29	43	72.9	170	2	Q921A6 mus musculus
30	43	72.9	321	2	Q921A6 mus musculus
31	43	72.9	475	2	Q921A6 mus musculus

32	43	72.9	484	2	Q921A6	Q921A6 mus musculus
33	43	72.9	487	2	Q921A6	Q921A6 mus musculus
34	42	71.2	121	1	Q921A6	Q921A6 mus musculus
35	42	71.2	129	2	Q921A6	Q921A6 mus musculus
36	42	71.2	129	2	Q921A6	Q921A6 mus musculus
37	41	69.5	113	2	Q921A6	Q921A6 mus musculus
38	41	69.5	117	1	Q921A6	Q921A6 mus musculus
39	41	69.5	117	1	Q921A6	Q921A6 mus musculus
40	41	69.5	117	1	Q921A6	Q921A6 mus musculus
41	41	69.5	117	1	Q921A6	Q921A6 mus musculus
42	41	69.5	117	1	Q921A6	Q921A6 mus musculus
43	41	69.5	117	1	Q921A6	Q921A6 mus musculus
44	41	69.5	119	2	Q921A6	Q921A6 mus musculus
45	41	69.5	120	2	Q921A6	Q921A6 mus musculus
46	41	69.5	137	2	Q921A6	Q921A6 mus musculus
47	41	69.5	139	1	Q921A6	Q921A6 mus musculus
48	41	69.5	139	1	Q921A6	Q921A6 mus musculus
49	41	69.5	140	2	Q921A6	Q921A6 mus musculus
50	41	69.5	140	2	Q921A6	Q921A6 mus musculus
51	41	69.5	141	2	Q921A6	Q921A6 mus musculus
52	41	69.5	142	2	Q921A6	Q921A6 mus musculus
53	41	69.5	143	2	Q921A6	Q921A6 mus musculus
54	41	69.5	143	2	Q921A6	Q921A6 mus musculus
55	41	69.5	143	2	Q921A6	Q921A6 mus musculus
56	41	69.5	143	2	Q921A6	Q921A6 mus musculus
57	41	69.5	143	2	Q921A6	Q921A6 mus musculus
58	41	69.5	144	2	Q921A6	Q921A6 mus musculus
59	41	69.5	144	2	Q921A6	Q921A6 mus musculus
60	41	69.5	145	2	Q921A6	Q921A6 mus musculus
61	41	69.5	145	2	Q921A6	Q921A6 mus musculus
62	41	69.5	145	2	Q921A6	Q921A6 mus musculus
63	41	69.5	145	2	Q921A6	Q921A6 mus musculus
64	41	69.5	145	2	Q921A6	Q921A6 mus musculus
65	41	69.5	145	2	Q921A6	Q921A6 mus musculus
66	41	69.5	145	2	Q921A6	Q921A6 mus musculus
67	41	69.5	146	2	Q921A6	Q921A6 mus musculus
68	41	69.5	146	2	Q921A6	Q921A6 mus musculus
69	41	69.5	240	2	Q921A6	Q921A6 mus musculus
70	41	69.5	255	2	Q921A6	Q921A6 mus musculus
71	41	69.5	422	2	Q921A6	Q921A6 mus musculus
72	41	69.5	473	2	Q921A6	Q921A6 mus musculus
73	41	69.5	473	2	Q921A6	Q921A6 mus musculus
74	41	69.5	482	2	Q921A6	Q921A6 mus musculus
75	41	69.5	482	2	Q921A6	Q921A6 mus musculus
76	41	69.5	488	2	Q921A6	Q921A6 mus musculus
77	41	69.5	488	2	Q921A6	Q921A6 mus musculus
78	41	69.5	488	2	Q921A6	Q921A6 mus musculus
79	41	69.5	488	2	Q921A6	Q921A6 mus musculus
80	41	69.5	488	2	Q921A6	Q921A6 mus musculus
81	41	69.5	488	2	Q921A6	Q921A6 mus musculus
82	41	69.5	488	2	Q921A6	Q921A6 mus musculus
83	41	69.5	488	2	Q921A6	Q921A6 mus musculus
84	41	69.5	488	2	Q921A6	Q921A6 mus musculus
85	41	69.5	488	2	Q921A6	Q921A6 mus musculus
86	41	69.5	488	2	Q921A6	Q921A6 mus musculus
87	41	69.5	488	2	Q921A6	Q921A6 mus musculus
88	41	69.5	488	2	Q921A6	Q921A6 mus musculus
89	41	69.5	488	2	Q921A6	Q921A6 mus musculus
90	41	69.5	488	2	Q921A6	Q921A6 mus musculus
91	41	69.5	488	2	Q921A6	Q921A6 mus musculus
92	41	69.5	488	2	Q921A6	Q921A6 mus musculus
93	41	69.5	488	2	Q921A6	Q921A6 mus musculus
94	41	69.5	488	2	Q921A6	Q921A6 mus musculus
95	41	69.5	488	2	Q921A6	Q921A6 mus musculus
96	41	69.5	488	2	Q921A6	Q921A6 mus musculus
97	41	69.5	488	2	Q921A6	Q921A6 mus musculus
98	41	69.5	488	2	Q921A6	Q921A6 mus musculus
99	41	69.5	488	2	Q921A6	Q921A6 mus musculus
100	41	69.5	488	2	Q921A6	Q921A6 mus musculus

ALIGNMENTS

```
RESULT 1
ID HV02_MOUSE PRELIMINARY; PRT; 241 AA.
AC 0921A6
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE 01-MAR-2004 (TREMblrel. 26, Last annotation update)
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scfv).";
RL Mol. Cells 7:816-819 (1997).
DR EMBL; U88067; AAB48044.1; -.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; 1BWW.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 91.5%; Score 54; DB 2; Length 241;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGMN 10
Db 26 GYFTDYGMN 35

RESULT 2
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8131846; PubMed=6186498;
RA Sikevitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idioType response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032 (1982).
CC -1- MISCELLANEOUS: From analysis of the sizes of several other
CC differentiatd genes that hybridize to this one, the authors
CC conclude that all of these V regions have rearranged to the same J
CC segment, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PDB; 1JFO; X-ray; H=1-120.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
```

```
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 111
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 84.7%; Score 50; DB 1; Length 120;
Best Local Similarity 80.0%; Pred. No. 0.33;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGMN 10
Db 25 GYFTSYGIN 34

RESULT 3
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RX MEDLINE=92152918; PubMed=6801765;
RA Sims J., Rabbits T.H., Bates P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "A somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311 (1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00493; AAA38128.1; -.
DR PIR; A94264; HWMSG7.
DR HSSP; P01747; 1JFO.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Hybridoma; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140
FT DOMAIN 20 139
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CB831DA5C88 CRC64;

Query Match 84.7%; Score 50; DB 1; Length 140;
Best Local Similarity 80.0%; Pred. No. 0.38;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGMN 10
Db 45 GYFTSYGIN 54

RESULT 4
ID Q6PIL0 PRELIMINARY; PRT; 125 AA.
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 129.094 Seconds
(without alignments)
50.931 Million cell updates/sec

Title: US-10-018-245A-2
Perfect score: 101
Sequence: 1 WINTYGEPTVADDFKG 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database :

1: A_Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	17	5	AAG80312
2	101	100.0	17	8	ADS87337
3	101	100.0	19	2	AAV17490
4	101	100.0	19	2	AAV08699
5	101	100.0	19	3	AAV83642
6	101	100.0	67	7	ADH62639
7	101	100.0	70	7	ADH62638
8	101	100.0	112	7	ADC27441
9	101	100.0	112	7	ADC27449
10	101	100.0	115	4	AAAB84740
11	101	100.0	116	4	AAAB84739
12	101	100.0	116	5	AAE27830
13	101	100.0	116	5	AAE27839
14	101	100.0	116	5	AAE27837
15	101	100.0	116	5	AAE27825
16	101	100.0	116	5	AAE27826
17	101	100.0	116	5	AAE27828
18	101	100.0	116	5	AAE27832
19	101	100.0	116	5	AAE27834
20	101	100.0	116	5	ADG67541
21	101	100.0	116	5	ADG67537
22	101	100.0	116	5	ADG67543
23	101	100.0	116	5	ADG67531
24	101	100.0	116	5	ADG67533
25	101	100.0	116	5	ADG67539

26	101	100.0	116	5	ADG67529	Adg67529 KS antibo
27	101	100.0	116	5	ADG67535	Adg67535 KS antibo
28	101	100.0	116	6	AAE33431	AAE33431 Murine KS
29	101	100.0	116	6	AAE33433	AAE33433 Murine KS
30	101	100.0	116	6	AAE33434	AAE33434 Murine KS
31	101	100.0	116	6	AAE33435	AAE33435 Murine KS
32	101	100.0	116	6	AAE33414	AAE33414 Murine KS
33	101	100.0	116	6	AAE33432	AAE33432 Murine KS
34	101	100.0	116	6	AAE33438	AAE33438 Murine KS
35	101	100.0	116	6	AAE33430	AAE33430 Murine KS
36	101	100.0	116	6	AAE33437	AAE33437 Murine KS
37	101	100.0	116	6	AAE33436	AAE33436 Murine KS
38	101	100.0	116	6	AAO30908	AAO30908 hu-KS ant
39	101	100.0	116	6	AAO30911	AAO30911 di-KS ant
40	101	100.0	117	2	AAE28752	AAE28752 Heavy cha
41	101	100.0	117	5	AAE80317	AAE80317 Anti-huma
42	101	100.0	117	6	AAE33439	AAE33439 Murine KS
43	101	100.0	118	2	AAE25414	AAE25414 Heavy cha
44	101	100.0	118	8	ADN16150	ADN16150 Mouse C7
45	101	100.0	119	3	AAE11995	AAE11995 Anti-11-d
46	101	100.0	119	6	AAO23065	AAO23065 Murine K8
47	101	100.0	122	8	ADS87370	ADS87370 ChimERIC
48	101	100.0	122	8	ADS87366	ADS87366 Murine MN
49	101	100.0	123	4	AAE98664	AAE98664 Murine pr
50	101	100.0	126	2	AAE17495	AAE17495 Heavy cha
51	101	100.0	137	5	AAE29158	AAE29158 ChimERIC
52	101	100.0	138	6	AAO23064	AAO23064 Murine K8
53	101	100.0	138	7	ABR62341	ABR62341 Anti-HLA-
54	101	100.0	139	2	AAO9428	AAO9428 KM10 Heav
55	101	100.0	139	2	AAO6217	AAO6217 Mab KM10
56	101	100.0	139	2	AAE85064	AAE85064 Mouse KM1
57	101	100.0	139	6	ABU58898	ABU58898 Mouse ant
58	101	100.0	141	8	ADS87374	ADS87374 Humanised
59	101	100.0	240	8	ADN16154	ADN16154 Mouse C7
60	101	100.0	242	4	AAE20433	AAE20433 Anti-FTX/
61	101	100.0	259	7	ADG32324	ADG32324 Mouse scf
62	101	100.0	259	7	ADG32322	ADG32322 Mouse scf
63	101	100.0	329	7	ADG32359	ADG32359 Precursor
64	101	100.0	329	7	ADG32361	ADG32361 Precursor
65	101	100.0	447	1	AAE93037	AAE93037 ChimERIC
66	101	100.0	579	6	AAE33444	AAE33444 KS antibo
67	101	100.0	579	6	AAO30910	AAO30910 di-KS-ala
68	98	97.0	160	4	AAE35101	AAE35101 Antibody
69	98	97.0	183	1	AAE70625	AAE70625 Sequence
70	98	97.0	183	1	AAE82936	AAE82936 Variable
71	98	97.0	183	1	AAE82938	AAE82938 Variable
72	98	97.0	183	1	AAE82939	AAE82939 Variable
73	98	97.0	183	1	AAE94778	AAE94778 V region
74	98	97.0	183	2	AAE10240	AAE10240 Variable
75	98	97.0	183	2	AAE10586	AAE10586 V region
76	98	97.0	183	2	AAE16341	AAE16341 L6 antibo
77	98	97.0	183	2	AAE41068	AAE41068 Mouse L6
78	98	97.0	183	2	AAE47511	AAE47511 Mouse L6
79	98	97.0	183	2	AAE47518	AAE47518 Mouse L6
80	98	97.0	183	2	AAE89536	AAE89536 Anti-canc
81	98	97.0	183	4	AAE98087	AAE98087 L6 VH CDN
82	98	97.0	183	4	ADC65008	ADC65008 Immunoglo
83	98	97.0	252	3	AAE12562	AAE12562 ChimERIC
84	98	97.0	252	3	AAE36825	AAE36825 L6 sfv pr
85	97	96.0	120	7	ABR61521	ABR61521 Humanised
86	97	96.0	120	7	ABR61521	ABR61521 Murine RS
87	97	96.0	121	7	ABR61525	ABR61525 Humanised
88	97	96.0	121	7	ABR61529	ABR61529 Humanised
89	97	96.0	121	7	ABR61527	ABR61527 Humanised
90	97	96.0	121	7	ABR61527	ABR61527 Humanised
91	97	96.0	121	7	ABR61527	ABR61527 Humanised
92	97	96.0	121	7	ABR61527	ABR61527 Humanised
93	97	96.0	121	7	ABR61527	ABR61527 Humanised
94	96	95.0	118	2	AAE38615	AAE38615 Low-risk
95	96	95.0	118	2	AAE38615	AAE38615 Humanised
96	96	95.0	118	2	AAE38615	AAE38615 Humanised
97	96	95.0	118	2	AAE38615	AAE38615 Humanised
98	96	95.0	118	2	AAE38615	AAE38615 Humanised
99	96	95.0	118	2	AAE38615	AAE38615 Humanised
100	96	95.0	118	2	AAE38615	AAE38615 Humanised

99 96 95.0 118 8 ADI01229
100 96 95.0 118 8 ADI01170

Adi01229 Murine mo
Adi01170 Murine mo

ALIGNMENTS

RESULT 1

AAG80312
ID AAG80312 standard; peptide; 17 AA.

AC AAG80312;

XX 18-FEB-2002 (first entry)

XX Anti-human TNF-alpha CDR-H2 peptide.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;

KW heavy chain; light chain; complementarity determining region; vasotropic;

KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;

XX rheumatoid arthritis; malaria; multiple sclerosis.

OS Homo sapiens.

XX WO200179298-A1.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-JP003308.

XX 19-APR-2000; 2000JP-00117394.

XX (SUNR) SUNTORY LTD.

XX Fukuda Y, Nagahira K, Nakanishi T;

XX WPI; 2002-066345/09.

XX Novel heavy and light-chain polypeptides of chimeric and humanized

PT antibodies against human tumor necrosis factor alpha for low-

PT immunogenicity treatment of TNF-related diseases such as toxic shock

PT syndrome.

XX Claim 1b; Page 25; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides

CC or their fragments of a recombinant antibody to human TNF-alpha which

CC contain complementarity determining region (CDR) sequences. The products

CC of the invention have vasotropic, antiarthritic, neuroprotective and

CC protozoacide activity. The antibodies act by neutralising TNF-alpha in

CC vivo. The antibodies are used for producing chimeric and humanised

CC antibodies that may be used for the treatment and prevention of TNF-alpha

CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,

CC malaria and multiple sclerosis. The antibodies have low immunogenicity in

CC human. This sequence represents the anti-human tumour necrosis factor-

CC alpha (TNF-alpha) heavy chain CDR1 designated CDR-H2

XX Sequence 17 AA;

XX Query Match 100.0%; Score 101; DB 5; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 2.4e-08;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 WINTYTGEPTYADDFKG 17

XX 1 WINTYTGEPTYADDFKG 17

XX RESULT 2

XX ADS87337 standard; peptide; 17 AA.

XX ADS87337;

XX AC ADS87337;

XX 18-NOV-2004 (first entry)

XX Humanised antibody MN3 heavy chain variable region CDR2.

XX Cytostatic; vasotropic; antimicrobial; antiinflammatory; antipyloric;

KW antiatherosclerotic; cardiant; monoclonal antibody; NCA90; NCA95;

KW chimeric antibody; humanized antibody; inflammation; appendicitis;

KW inflammatory bowel disease; pelvic inflammatory disease; fever;

KW cystic fibrosis; granulocyte related disorder; atherosclerosis;

KW infarction; cancer; ischemic lesion; complementarity determining region.

XX Homo sapiens.

XX Mus sp.

XX Chimeric.

XX WO2004029093-A2.

XX 08-APR-2004.

XX 30-SEP-2003; 2003WO-GB0044229.

XX 30-SEP-2002; 2002US-0414341P.

XX (IMMU-) IMMUNOMEDICS INC.

XX (MCCA/) MCCAAL J D.

XX Goldenberg DM, Hansen H, Leung S;

XX WPI; 2004-329873/30.

XX Monoclonal anti-granulocyte antibody that binds NCA90 and NCA95 antigens,

PT useful for treating malignancy, inflammation, atherosclerosis,

PT infarction, or other granulocyte related disorders.

XX Claim 4; Page 105; 134pp; English.

XX The invention relates to a monoclonal antibody (Mab) (I) or its fragment

CC that binds NCA90 or NCA95, where when the Mab or its fragment binds NCA90

CC the Mab or its fragment is chimeric, partially humanized or fully

CC humanized and where when the Mab or its fragment binds NCA95 the Mab or

CC its fragment is either fully humanized or chimeric, partially humanized

CC or fully humanized BW 250/183. (I) is useful for treating, detecting or

CC imaging sites of inflammation resulting from appendicitis, inflammatory

CC bowel disease, pelvic inflammatory disease, fever and cystic fibrosis and

CC treating granulocyte related disorders, atherosclerosis and infarction.

CC (I) is useful for detecting or treating cancer or ischemic lesion. This

CC sequence corresponds to the complementarity determining region 2 (CDR2)

CC of the heavy chain of the antibody of the invention.

XX Sequence 17 AA;

XX Query Match 100.0%; Score 101; DB 8; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 2.4e-08;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 WINTYTGEPTYADDFKG 17

XX 1 WINTYTGEPTYADDFKG 17

XX RESULT 3

XX AA17490 standard; peptide; 19 AA.

XX AA17490

XX AA17490;

XX 03-AUG-1999 (first entry)

XX Mab 31.1 CDR sequence derived peptide COL311 H2.

XX Heavy chain variable region; 2CAVHC0L1; light chain variable region;

XX light chain consensus region; heavy chain consensus region; antibody;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:57:11 ; Search time 34.2656 Seconds
(without alignments)
37.035 Million cell updates/sec

Title: US-10-018-245A-2
Perfect score: 101
Sequence: 1 WINTYGEPTVADDFKG 17

Scoring table: BLOSUM62
Gap 10.0 , Gape 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCITUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	98	97.0	160	4 US-09-318-786-35	Sequence 35, Appl
2	98	97.0	252	3 US-08-279-772A-6	Sequence 6, Appl
3	98	97.0	252	3 US-08-902-486-9	Sequence 9, Appl
4	96	95.0	118	1 US-08-435-336-124	Sequence 124, App
5	96	95.0	118	1 US-08-488-113B-124	Sequence 124, App
6	96	95.0	118	1 US-08-477-484B-124	Sequence 124, App
7	96	95.0	118	1 US-08-107-669D-28	Sequence 28, Appl
8	96	95.0	118	1 US-08-107-669D-29	Sequence 29, Appl
9	96	95.0	118	1 US-08-107-669D-66	Sequence 66, Appl
10	96	95.0	118	1 US-08-472-788A-28	Sequence 28, Appl
11	96	95.0	118	1 US-08-472-788A-29	Sequence 29, Appl
12	96	95.0	118	1 US-08-472-788A-88	Sequence 88, Appl
13	96	95.0	118	2 US-08-477-531B-28	Sequence 28, Appl
14	96	95.0	118	2 US-08-477-531B-29	Sequence 29, Appl
15	96	95.0	118	2 US-08-477-531B-66	Sequence 66, Appl
16	96	95.0	118	2 US-08-646-360-124	Sequence 124, App
17	96	95.0	118	2 US-08-082-842A-28	Sequence 28, Appl
18	96	95.0	118	2 US-08-082-842A-29	Sequence 29, Appl
19	96	95.0	118	2 US-08-082-842A-88	Sequence 88, Appl
20	96	95.0	118	3 US-08-839-765-124	Sequence 124, App
21	96	95.0	118	3 US-09-136-389-124	Sequence 124, App
22	96	95.0	118	3 US-09-610-838-124	Sequence 124, App
23	96	95.0	118	4 US-09-711-485-124	Sequence 124, App
24	93	92.1	140	3 US-08-569-147-76	Sequence 76, Appl
25	93	92.1	140	3 US-08-569-147-82	Sequence 82, Appl
26	93	92.1	365	3 US-08-875-811-53	Sequence 53, Appl
27	93	92.1	366	3 US-08-875-811-55	Sequence 55, Appl

28	92	91.1	136	3 US-09-184-658-32	Sequence 32, Appl
29	92	91.1	136	4 US-09-504-262D-32	Sequence 32, Appl
30	92	91.1	259	4 US-09-419-788-115	Sequence 115, App
31	92	91.1	278	3 US-09-184-658-47	Sequence 47, Appl
32	92	91.1	278	4 US-09-504-262D-47	Sequence 47, Appl
33	92	91.1	284	3 US-09-184-658-40	Sequence 40, Appl
34	92	91.1	284	4 US-09-504-262D-40	Sequence 40, Appl
35	91	90.1	119	4 US-09-232-290-50	Sequence 50, Appl
36	90	89.1	118	1 US-08-425-336-126	Sequence 126, App
37	90	89.1	118	1 US-08-488-113B-126	Sequence 126, App
38	90	89.1	118	1 US-08-477-484B-126	Sequence 126, App
39	90	89.1	118	1 US-08-107-669D-67	Sequence 67, Appl
40	90	89.1	118	1 US-08-472-788A-89	Sequence 89, Appl
41	90	89.1	118	2 US-08-477-531B-67	Sequence 67, Appl
42	90	89.1	118	2 US-08-646-360-126	Sequence 126, App
43	90	89.1	118	2 US-08-082-842A-89	Sequence 89, Appl
44	90	89.1	118	3 US-08-839-765-126	Sequence 126, App
45	90	89.1	118	3 US-09-136-389-126	Sequence 126, App
46	90	89.1	118	3 US-09-610-838-126	Sequence 126, App
47	90	89.1	118	4 US-09-711-485-126	Sequence 126, App
48	90	89.1	240	1 US-08-488-113B-147	Sequence 147, App
49	90	89.1	240	1 US-08-477-484B-147	Sequence 147, App
50	90	89.1	240	1 US-08-477-484B-148	Sequence 148, App
51	90	89.1	240	2 US-08-646-360-147	Sequence 147, App
52	90	89.1	240	2 US-08-646-360-148	Sequence 148, App
53	90	89.1	240	2 US-08-646-360-148	Sequence 148, App
54	90	89.1	240	3 US-08-839-765-147	Sequence 147, App
55	90	89.1	240	3 US-08-839-765-148	Sequence 148, App
56	90	89.1	240	3 US-09-136-389-147	Sequence 147, App
57	90	89.1	240	3 US-09-136-389-148	Sequence 148, App
58	90	89.1	240	3 US-09-610-838-147	Sequence 147, App
59	90	89.1	240	3 US-09-610-838-148	Sequence 148, App
60	90	89.1	240	4 US-09-711-485-147	Sequence 147, App
61	90	89.1	240	4 US-09-711-485-148	Sequence 148, App
62	89	88.1	230	3 US-09-485-737B-102	Sequence 102, App
63	89	88.1	230	4 US-10-071-485-102	Sequence 102, App
64	89	88.1	235	3 US-09-485-737B-93	Sequence 93, Appl
65	89	88.1	235	4 US-10-071-485-93	Sequence 93, Appl
66	89	88.1	240	3 US-09-485-737B-91	Sequence 91, Appl
67	89	88.1	240	4 US-10-071-485-91	Sequence 91, Appl
68	89	88.1	267	3 US-09-485-737B-2	Sequence 2, Appl
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75	89	88.1	711	4 US-10-071-485-90	Sequence 90, Appl
76	87	86.1	118	4 US-09-440-781-96	Sequence 96, Appl
77	87	86.1	118	4 US-09-440-781-97	Sequence 97, Appl
78	87	86.1	121	4 US-09-440-781-98	Sequence 98, Appl
79	87	86.1	121	4 US-09-440-781-99	Sequence 99, Appl
80	87	86.1	491	4 US-10-011-125A-2	Sequence 2, Appl
81	84	83.2	115	3 US-08-483-749A-24	Sequence 24, Appl
82	84	83.2	243	1 US-08-133-804-6	Sequence 6, Appl
83	84	83.2	243	2 US-08-461-838-6	Sequence 6, Appl
84	84	83.2	243	2 US-08-461-838-6	Sequence 6, Appl
85	84	83.2	243	2 US-08-356-786-4	Sequence 4, Appl
86	84	83.2	250	1 US-08-133-804-2	Sequence 2, Appl
87	84	83.2	250	1 US-08-461-838-8	Sequence 8, Appl
88	84	83.2	250	1 US-08-463-675-8	Sequence 8, Appl
89	84	83.2	250	1 US-08-463-675-8	Sequence 8, Appl
90	84	83.2	250	1 US-08-464-589-8	Sequence 8, Appl
91	84	83.2	250	1 US-08-461-838-2	Sequence 2, Appl
92	84	83.2	250	2 US-08-461-838-2	Sequence 2, Appl
93	84	83.2	534	2 US-08-356-786-16	Sequence 16, Appl
94	83	82.2	622	2 US-08-356-786-16	Sequence 16, Appl
95	83	82.2	17	1 US-08-438-123-5	Sequence 5, Appl
96	83	82.2	21	1 US-08-438-123-5	Sequence 5, Appl
97	83	82.2	148	1 US-08-438-123-3	Sequence 3, Appl
98	81	80.2	119	3 US-08-933-983-79	Sequence 79, Appl
99	81	80.2	141	3 US-08-933-983-81	Sequence 81, Appl
100	80	79.2	17	3 US-08-589-939-5	Sequence 5, Appl
				3 US-09-406-532-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-318-786-35

Sequence 35, Application US/09318786
Patent No. 6472147
GENERAL INFORMATION:
APPLICANT: Janda, Kim D
APPLICANT: Wirsching, Peter
APPLICANT: Lerner, Richard A
APPLICANT: Gao, Changshou
TITLE OF INVENTION: METHODS FOR DISPLAY OF HETERODIMERIC PROTEINS ON
FILAMENTOUS PHAGE USING PVI AND PIX, COMPOSITIONS,
TITLE OF INVENTION: VECTORS AND COMBINATORIAL LIBRARIES
FILE REFERENCE: TSR03055
CURRENT APPLICATION NUMBER: US/09/318,786
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 160
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: fusion
US-09-318-786-35

Query Match 97.0%; Score 98; DB 4; Length 160;
Best Local Similarity 94.1%; Pred. No. 1.8e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17

DB 52 WINTYGEPTVADDFRG 68

RESULT 2

US-08-279-772A-6

Sequence 6, Application US/08279772A
Patent No. 6080560
GENERAL INFORMATION:
APPLICANT: Russell, David R
APPLICANT: Fuller, James T
TITLE OF INVENTION: Method for Producing Antibodies in Plant
TITLE OF INVENTION: Cells
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
STREET: PO Box 2113
CITY: Madison
STATE: WI
COUNTRY: United States of America
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,772A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9097-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-279-772A-6

Query Match 97.0%; Score 98; DB 3; Length 252;
Best Local Similarity 94.1%; Pred. No. 2.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17

DB 180 WINTYGOPTVADDFKG 196

RESULT 3

US-08-902-486-9

Sequence 9, Application US/08902486
Patent No. 6140075
GENERAL INFORMATION:
APPLICANT: Russell, David R.
APPLICANT: Fuller, James T.
TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
PROTEIN TOXINS IN PLANT CELLS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,486
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 670513.90261
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-902-486-9

Query Match 97.0%; Score 98; DB 3; Length 252;
Best Local Similarity 94.1%; Pred. No. 2.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17

DB 180 WINTYGOPTVADDFKG 196

RESULT 4

US-08-425-336-124

Sequence 124, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:56:15 ; Search time 98.0156 Seconds
(without alignments)
57.427 Million cell updates/sec

Title: US-10-018-245A-2
Perfect score: 101
Sequence: 1 WINTYGEPTAYADFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	101	100.0	17	16	US-10-018-245A-2
3	101	100.0	67	14	US-10-243-130-19
4	101	100.0	70	14	US-10-243-130-17
5	101	100.0	70	14	US-10-243-130-18
6	101	100.0	70	14	US-10-901-650-17
7	101	100.0	70	17	US-10-901-650-18
8	101	100.0	70	17	US-10-901-650-19
9	101	100.0	112	15	US-10-383-447-10
10	101	100.0	112	15	US-10-383-447-18
11	101	100.0	116	14	US-10-138-727A-2
12	101	100.0	116	14	US-10-138-727A-18
13	101	100.0	116	14	US-10-138-727A-19

14	101	100.0	116	14	US-10-138-727A-20	Sequence 20, Appl
15	101	100.0	116	14	US-10-138-727A-21	Sequence 21, Appl
16	101	100.0	116	14	US-10-138-727A-22	Sequence 22, Appl
17	101	100.0	116	14	US-10-138-727A-23	Sequence 23, Appl
18	101	100.0	116	14	US-10-138-727A-24	Sequence 24, Appl
19	101	100.0	116	14	US-10-138-727A-25	Sequence 25, Appl
20	101	100.0	116	14	US-10-138-727A-26	Sequence 26, Appl
21	101	100.0	116	14	US-10-138-727A-27	Sequence 27, Appl
22	101	100.0	116	14	US-10-138-727A-28	Sequence 28, Appl
23	101	100.0	116	14	US-10-138-727A-29	Sequence 29, Appl
24	101	100.0	116	14	US-10-138-727A-30	Sequence 30, Appl
25	101	100.0	116	14	US-10-138-727A-31	Sequence 31, Appl
26	101	100.0	116	14	US-10-138-727A-32	Sequence 32, Appl
27	101	100.0	116	14	US-10-138-727A-33	Sequence 33, Appl
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35	101	100.0	116	14	US-10-138-727A-41	Sequence 41, Appl
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87 89 88.1 123 16 US-10-723-434-106 Sequence 106, App
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89 89 88.1 235 14 US-10-071-485-93 Sequence 93, App
90 89 88.1 240 14 US-10-071-485-91 Sequence 91, App
91 89 88.1 267 14 US-10-071-485-2 Sequence 8, App
92 89 88.1 465 15 US-10-404-724-8 Sequence 23, App
93 89 88.1 465 17 US-10-816-276-4 Sequence 4, App
94 89 88.1 465 17 US-10-816-276-19 Sequence 19, App
95 89 88.1 468 14 US-10-071-485-67 Sequence 67, App
96 89 88.1 541 14 US-10-071-485-85 Sequence 85, App
97 89 88.1 711 14 US-10-071-485-90 Sequence 90, App
98 89 88.1 116 14 US-10-138-727A-4 Sequence 4, App
99 88 87.1 116 14 US-10-138-727A-4 Sequence 6, App
100 88 87.1 116 14 US-10-138-727A-6 Sequence 6, App

ALIGNMENTS

RESULT 1
US-09-791-551-86

Sequence 86, Application US/09791551
Publication No. US20030235584A1

GENERAL INFORMATION:

APPLICANT: KLOETZER, WILLIAM S.

APPLICANT: HANNA, NABIL

TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES

FILE REFERENCE: 037003/0277869

CURRENT APPLICATION NUMBER: US/09/791,551

CURRENT FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: 60/185,390

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: 60/233,625

PRIOR FILING DATE: 2000-09-18

NUMBER OF SEQ ID NOS: 119

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 86

LENGTH: 17

TYPE: PRT

ORGANISM: Mus sp.

US-09-791-551-86
Query Match 100.0%; Score 101; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1,6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGEPTYADDFKG 17
Db 1 WINTYGEPTYADDFKG 17

RESULT 2

US-10-018-245A-2

Sequence 2, Application US/10018245A

Publication No. US20040115196A1

GENERAL INFORMATION:

APPLICANT: FUKUDA, Yoshiaki

APPLICANT: NAGAHARA, Kazuhiro

APPLICANT: NAKANISHI, Toshihiro

TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement

FILE REFERENCE: 46224

CURRENT APPLICATION NUMBER: US/10/018,245A

CURRENT FILING DATE: 2002-07-12

PRIOR APPLICATION NUMBER: JP 117394/2000

PRIOR FILING DATE: 2000-04-19

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 17

TYPE: PRT

ORGANISM: mouse

FEATURE:

OTHER INFORMATION: CDR-H2 of anti-human TNF-alpha antibody
US-10-018-245A-2

Query Match 100.0%; Score 101; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 1,6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 WINTYGEPTYADDFKG 17

RESULT 3

US-10-243-130-19

Sequence 19, Application US/10243130

Publication No. US20030143682A1

GENERAL INFORMATION:

APPLICANT: Nicolaides, Nicholas C.

APPLICANT: Grasso, Luigi

TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED

FILE REFERENCE: MOR-130

CURRENT APPLICATION NUMBER: US/10/243,130

CURRENT FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: 09/707,468

PRIOR FILING DATE: 2000-11-07

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.2

SEQ ID NO 19

LENGTH: 67

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Consensus sequence

US-10-243-130-19
Query Match 100.0%; Score 101; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 6,4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGEPTYADDFKG 17
Db 44 WINTYGEPTYADDFKG 60

RESULT 4

US-10-243-130-17

Sequence 17, Application US/10243130

Publication No. US20030143682A1

GENERAL INFORMATION:

APPLICANT: Nicolaides, Nicholas C.

APPLICANT: Grasso, Luigi

TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED

FILE REFERENCE: MOR-130

CURRENT APPLICATION NUMBER: US/10/243,130

CURRENT FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: 09/707,468

PRIOR FILING DATE: 2000-11-07

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.2

SEQ ID NO 17

LENGTH: 70

TYPE: PRT

ORGANISM: Homo sapiens

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Best Local Similarity 100.0%; Pred. No. 6,7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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Run on: March 24, 2005, 08:54:18 ; Search time 404.547 Seconds
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Title: US-10-018-245A-2
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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72	101	100.0	116	30	US-10-468-370-668	Sequence 668, App
73	101	100.0	116	30	US-10-468-370-670	Sequence 670, App
74	101	100.0	116	30	US-10-468-370-672	Sequence 672, App
75	101	100.0	116	30	US-10-468-496-2021	Sequence 2021, Ap
76	101	100.0	116	30	US-10-468-496-2023	Sequence 2023, Ap
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89	101	100.0	117	16	US-09-267-281-20	Sequence 20, Appl
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91	101	100.0	117	27	US-10-138-727A-35	Sequence 35, Appl
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93	101	100.0	118	6	US-08-292-866-23	Sequence 23, Appl
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95	101	100.0	118	13	US-08-924-754-23	Sequence 23, Appl
96	101	100.0	118	13	US-08-924-796-23	Sequence 23, Appl
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98	101	100.0	118	16	US-09-267-281-19	Sequence 19, Appl
99	101	100.0	118	22	US-09-791-537-55585	Sequence 55585, A
100	101	100.0	118	30	US-10-422-049-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-791-551-86
Sequence 86, Application US/09791551
GENERAL INFORMATION:
APPLICANT: KLOETZER, WILLIAM S.
APPLICANT: HANNA, NABIL
TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
FILE REFERENCE: 037003/0277869
CURRENT APPLICATION NUMBER: US/09/791,551
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/185,390
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/233,625
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 119
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 17
TYPE: PRT
ORGANISM: Mus sp.
US-09-791-551-86

Query Match 100.0%; Score 101; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 9,3e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGEPTYADDFKG 17
Db 1 WINTYGEPTYADDFKG 17

RESULT 2
US-10-018-245A-2
Sequence 2, Application US/10018245A
GENERAL INFORMATION:
APPLICANT: FUKUDA, Yoshiaki
APPLICANT: NAGAHARA, Kazuhito

APPLICANT: NAKANISHI, Toshihiro
TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
TITLE OF INVENTION: determining regions and genes encoding the same
FILE REFERENCE: 46224
CURRENT APPLICATION NUMBER: US/10/018,245A
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: JP 117394/2000
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 17
TYPE: PRT
ORGANISM: mouse
FEATURE:
OTHER INFORMATION: CDR-H2 of anti-human TNF-alpha antibody
US-10-018-245A-2

Query Match 100.0%; Score 101; DB 26; Length 17;
Best Local Similarity 100.0%; Pred. No. 9,3e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGEPTYADDFKG 17
Db 1 WINTYGEPTYADDFKG 17

RESULT 3
US-10-672-278-5
Sequence 5, Application US/10672278
GENERAL INFORMATION:
APPLICANT: GOLDBERG, DAVID M.
APPLICANT: HANSEN, HANS J.
APPLICANT: LEUNG, SHUI-ON
TITLE OF INVENTION: CHIMERIC, HUMAN AND HUMANIZED ANTI-GRANULOCYTE
TITLE OF INVENTION: ANTIBODIES AND METHODS OF USE
FILE REFERENCE: 40923-0134US1
CURRENT APPLICATION NUMBER: US/10/672,278
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: PCT/GB03/04229
PRIOR FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: 60/414,341
PRIOR FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 5
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Chimeric amino
US-10-672-278-5

Query Match 100.0%; Score 101; DB 32; Length 17;
Best Local Similarity 100.0%; Pred. No. 9,3e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGEPTYADDFKG 17
Db 1 WINTYGEPTYADDFKG 17

RESULT 4
PCT-US98-24302-14
Sequence 14, Application PC/TUS9824302
GENERAL INFORMATION:
APPLICANT: Purdie Pharma L.P.
TITLE OF INVENTION: IMMUNOGLOBULIN MOLECULES HAVING A SYNTHETIC VARIABLE
FILE REFERENCE: 6750-016-228
CURRENT APPLICATION NUMBER: PCT/US98/24302
CURRENT FILING DATE: 1998-11-13

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 23.9062 Seconds
(without alignments)
68.421 Million cell updates/sec

Title: US-10-018-245A-2
Perfect score: 101
Sequence: 1 WINTYGEPTVADDFK 17

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	101	2 D24672	Ig heavy chain V r
2	101	100.0	105	2 S24764	Ig heavy chain V r
3	101	100.0	105	2 S24765	Ig heavy chain V r
4	101	100.0	109	2 S26325	Ig heavy chain V r
5	101	100.0	118	2 S19967	Ig heavy chain V r
6	101	100.0	119	2 A53285	Ig heavy chain V a
7	101	100.0	124	2 PH1404	Ig heavy chain V r
8	98	97.0	115	2 S19968	Ig heavy chain V r
9	98	97.0	120	2 B42848	Ig heavy chain V r
10	98	97.0	146	4 S33905	Ig heavy chain pre
11	97	96.0	102	2 C32530	Ig heavy chain V r
12	92	91.1	105	2 S24766	Ig heavy chain V r
13	91	90.1	118	2 A32530	Ig heavy chain V r
14	90	89.1	114	2 D32967	Ig heavy chain V r
15	90	89.1	114	2 C32967	Ig heavy chain V r
16	90	89.1	117	2 S32187	Ig heavy chain V r
17	90	89.1	117	2 S32187	Ig heavy chain V r
18	89	88.1	136	2 S35759	Ig heavy chain V r
19	88	87.1	119	2 B32530	BHD9D10 protein -
20	86.5	85.6	119	2 H45722	anti-I-glycoprotein
21	86	85.1	113	2 B36259	Ig heavy chain V r
22	86	85.1	114	2 PL0256	Ig heavy chain V r
23	86	85.1	120	2 S19963	Ig heavy chain V r
24	86	85.1	139	2 PH1225	Ig heavy chain pre
25	84	83.2	93	2 C24672	Ig heavy chain V r
26	84	83.2	99	2 S26326	Ig heavy chain V r
27	83	82.2	115	2 S19965	Ig heavy chain V r
28	78	77.2	118	2 S37204	Ig heavy chain V r
29	75	74.3	120	2 S26789	Ig heavy chain V r

30	73	72.3	98	2 S46460	Ig heavy chain V r
31	73	72.3	105	2 S24763	Ig heavy chain V r
32	68	67.3	98	2 A49051	Ig heavy chain V7
33	68	67.3	117	2 S18554	Ig heavy chain V r
34	68	67.3	131	2 S26792	Ig heavy chain V r
35	64	63.4	142	2 S19245	Ig heavy chain pre
36	63	62.4	98	2 H34964	Ig heavy chain V-I
37	60	59.4	134	2 S21916	Ig heavy chain V r
38	53	52.5	86	2 S54912	Ig heavy chain V r
39	49	48.5	131	2 S21924	Ig heavy chain V r
40	49	48.5	160	2 PL0105	anti-PR2 erythrocy
41	47	46.5	98	2 PH0871	Ig heavy chain V r
42	47	46.5	123	2 D33548	Ig heavy chain V-I
43	46.5	46.0	415	2 AG0301	probable membrane
44	46.5	45.5	79	2 A49021	Ig heavy chain V-X
45	46	45.5	109	2 PH1668	Ig heavy chain V r
46	46	45.5	127	2 S34014	Ig heavy chain V r
47	46	45.5	127	2 B86165	Ig heavy chain V r
48	45.5	45.0	1020	2 T18260	1-phosphatidylinos
49	45	44.6	98	2 S26912	Ig heavy chain V r
50	45	44.6	98	2 S26938	Ig heavy chain V r
51	45	44.6	98	2 S26919	Ig heavy chain V r
52	45	44.6	111	2 S21925	Ig heavy chain V r
53	45	44.6	114	2 PH1667	Ig heavy chain V r
54	45	44.6	117	2 S31680	Ig heavy chain V r
55	45	44.6	117	2 S18551	Ig heavy chain V r
56	45	44.6	118	2 PH1666	Ig heavy chain V r
57	45	44.6	118	2 S36265	Ig heavy chain V r
58	45	44.6	122	2 S36271	Ig heavy chain V r
59	45	44.6	129	2 S36260	Ig heavy chain V r
60	45	44.6	129	2 S46393	Ig heavy chain V r
61	45	44.6	135	2 S49530	anti-Sm antibody V
62	45	44.6	143	2 AG2289	mutator protein [i
63	45	44.6	1842	2 T43409	probable fatty-aci
64	45	44.6	1842	2 T38781	fatty acid synthase
65	44	43.6	124	2 S19665	Ig heavy chain V r
66	44	43.6	136	1 HVM5B1	Ig heavy chain pre
67	44	43.6	213	2 I40576	hypothetical prote
68	44	43.6	367	2 T26291	hypothetical prote
69	44	43.6	412	2 S30299	Krox-20 protein -
70	44	43.6	446	2 S67437	Damage and replica
71	44	43.6	474	2 S66480	carbon catabolite
72	43.5	43.1	118	2 T09487	hypothetical prote
73	43.5	43.1	145	2 I47185	Ig heavy chain var
74	43	42.6	96	2 S17609	Ig heavy chain V r
75	43	42.6	143	1 E1H0ND	Ig heavy chain pre
76	43	42.6	201	2 A87680	RNA polymerase sig
77	43	42.6	258	2 I64070	cyclase hlsr H1047
78	43	42.6	381	2 AD0191	L-lactate dehydrog
79	43	42.6	434	2 AE3448	guanine deaminase
80	43	42.6	443	2 T21598	hypothetical prote
81	43	42.6	696	2 T02832	long chain fatty a
82	43	42.6	1071	2 T52306	methionine S-methy
83	43	42.6	1951	2 B43963	RNA viral polymera
84	43	42.6	2150	2 S13553	hypothetical prote
85	43	42.6	6486	2 T31076	tyrosinase synthet
86	42.5	42.1	120	1 G1HND	Ig heavy chain V-I
87	42.5	42.1	264	2 B1362	probable exodeoxyr
88	42.5	42.1	592	2 D70327	glutamine-fructose
89	42	41.6	98	2 S26918	Ig heavy chain V r
90	42	41.6	98	2 S17604	Ig heavy chain V r
91	42	41.6	110	2 PH1670	Ig heavy chain V r
92	42	41.6	114	2 S26319	Ig heavy chain V r
93	42	41.6	117	2 S18553	Ig heavy chain V r
94	42	41.6	118	2 S25174	Ig heavy chain V r
95	42	41.6	118	2 F72529	hypothetical prote
96	42	41.6	132	2 S31596	Ig heavy chain V r
97	42	41.6	135	2 PS0057	Ig heavy chain pre
98	42	41.6	136	2 S31600	Ig heavy chain V r
99	42	41.6	136	2 S04576	Ig heavy chain pre
100	42	41.6	155	2 T13308	hypothetical prote

ALIGNMENTS

RESULT 1

D24672

Ig heavy chain V region (VGM3-8) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C/Accession: D24672

R/Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A/Reference number: A91022; MUID:86055722; PMID:2998759

A/Accession: D24672

A/Molecule type: DNA

A/Residues: 1-101 <WIN>

A/Cross-references: GB:X03301; NID:951757; PIDN:CAA27040.1; PID:9773215

A/Note: this sequence was determined from the differentiated gene

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 101; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WINTYGEPTYADDFKG 17

Db 31 WINTYGEPTYADDFKG 47

RESULT 2

S24764

Ig heavy chain V region (subgroup XI) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999

C/Accession: S24764; S24772; S24777

R/Klages, S.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24763

A/Accession: S24764

A/Molecule type: DNA

A/Residues: 1-105 <KLA>

A/Cross-references: EMBL:Z14999

A/Accession: S24772

A/Molecule type: DNA

A/Residues: 1-105 <KLM>

A/Cross-references: EMBL:Z15011

R/Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24776

A/Accession: S24777

A/Molecule type: DNA

A/Residues: 1-105 <THO>

A/Cross-references: EMBL:Z15020; NID:952616; PIDN:CAA78739.1; PID:952617

C/Genetics: 9/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 101; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WINTYGEPTYADDFKG 17

Db 62 WINTYGEPTYADDFKG 78

RESULT 3

S24765

Ig heavy chain V region (subgroup XI) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999

C/Accession: S24765; S24773; S24778

R/Klages, S.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24763

A/Accession: S24765

A/Molecule type: DNA

A/Residues: 1-105 <KLA>

A/Cross-references: EMBL:Z15001

A/Accession: S24773

A/Molecule type: DNA

A/Residues: 1-105 <KLM>

A/Cross-references: EMBL:Z15013

R/Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24776

A/Accession: S24778

A/Molecule type: DNA

A/Residues: 1-105 <THO>

A/Cross-references: EMBL:Z15022; NID:952619; PIDN:CAA78741.1; PID:952620

C/Genetics: 9/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 101; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WINTYGEPTYADDFKG 17

Db 62 WINTYGEPTYADDFKG 78

RESULT 4

S26325

Ig heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S26325

R/Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a protein ef

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26325

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-109 <STA>

A/Cross-references: UNIPROT:Q921A6; EMBL:X59210; NID:952080; PID:91334043

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;5-88/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WINTYGEPTYADDFKG 17

Db 40 WINTYGEPTYADDFKG 56

RESULT 5

S19967

Ig heavy chain V region (M-T406) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C/Accession: S19967

R/Weissenhorn, W.; Riethmüller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A/Description: Structural characterization of CD4 mAb.

A/Reference number: S19963

A/Accession: S19967

A/Status: preliminary

A/Molecule type: mRNA

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 112.094 Seconds
(without alignments)
77.661 Million cell updates/sec

Title: US-10-018-245A-2
Perfect score: 101
Sequence: 1 WINTYGTGEPTVADDFKG 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

UniProt 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	101	100.0	241 2 Q921A6	Q921A6 mus musculus
2	92	91.1	102 2 Q91L79	Q91L79 mus musculus
3	87	86.1	116 2 Q683Y7	Q683Y7 mus musculus
4	87	86.1	116 2 Q683Y8	Q683Y8 mus musculus
5	86	85.1	140 2 Q652L3	Q652L3 mus sp. tgi
6	73	72.3	125 2 Q6PIL0	Q6PIL0 homo sapien
7	72	71.3	484 2 Q99LA6	Q99LA6 mus musculus
8	71	70.3	218 2 Q925S1	Q925S1 mus musculus
9	51	50.5	381 2 Q9GNT8	Q9GNT8 caenorhabdi
10	50	49.5	379 2 Q87G18	Q87G18 vibrio para
11	49	48.5	610 2 Q9HKK6	Q9HKK6 thermoplas
12	49	48.5	1549 2 Q76D19	Q76D19 clostridium
13	48	47.5	500 2 Q6N091	Q6N091 homo sapien
14	48	47.5	2009 2 Q7N8A8	Q7N8A8 photorhabd
15	48	47.5	2151 2 Q6B7Y9	Q6B7Y9 suchong vir
16	48	47.5	2992 2 Q7RXD7	Q7RXD7 neurospora
17	47	46.5	518 2 Q6N030	Q6N030 homo sapien
18	47	46.5	1085 2 Q852S0	Q852S0 thermotoga
19	46.5	46.0	414 2 Q669H4	Q669H4 yersinia ps
20	46.5	46.0	415 2 Q8ZDP6	Q8ZDP6 yersinia pe
21	46	45.5	154 2 Q6UP30	Q6UP30 chlamydomon
22	46	45.5	341 2 Q8ZWT8	Q8ZWT8 pyrobaculum
23	46	45.5	470 2 Q9ZVT6	Q9ZVT6 arabidopsis
24	45.5	45.0	244 2 Q6MX64	Q6MX64 azocarcus sp
25	45.5	45.0	1020 1 VP34 CANAL	Q92213 candida alb
26	45	44.6	143 2 Q8YOG1	Q8YOG1 anabaena sp
27	45	44.6	182 2 Q8GAB6	Q8GAB6 bifidobacte
28	45	44.6	389 2 Q752V2	Q752V2 asibya goss
29	45	44.6	411 2 Q6PPG2	Q6PPG2 chlamydomon
30	45	44.6	469 2 Q7Z7P5	Q7Z7P5 homo sapien
31	45	44.6	487 2 Q6QBS6	Q6QBS6 chlamydomon

32	45	44.6	507 2 P955S2	P955S2 pseudomonas
33	45	44.6	527 2 Q65FV7	Q65FV7 bacillus li
34	45	44.6	576 2 Q65WZ7	Q65WZ7 oryza sativ
35	45	44.6	745 2 Q6LZT9	Q6LZT9 methanococc
36	45	44.6	753 2 Q9EY04	Q9EY04 clostridium
37	45	44.6	759 2 Q8A3F1	Q8A3F1 bacteroides
38	45	44.6	868 2 Q8A2M9	Q8A2M9 bacteroides
39	45	44.6	1842 1 FAS2 SCHPO	Q10289 s fatty aci
40	44.5	44.1	191 2 Q9NUY2	Q9NUY2 gallardia lam
41	44.5	44.1	469 2 Q7XJ49	Q7XJ49 allium cepa
42	44	43.6	136 1 HV15 MOUSE	P01759 mus musculu
43	44	43.6	213 2 Q45776	Q45776 bacteroides
44	44	43.6	213 2 Q72AR7	Q72AR7 desulfotolvir
45	44	43.6	215 2 Q81HL9	Q81HL9 trophoblast
46	44	43.6	220 2 Q830L3	Q830L3 enterococcu
47	44	43.6	310 2 Q9APR2	Q9APR2 oryza sativ
48	44	43.6	353 2 Q8L0J3	Q8L0J3 uncultured
49	44	43.6	366 2 Q8V091	Q8V091 uncultured
50	44	43.6	367 2 Q7YTW2	Q7YTW2 caenorhabdi
51	44	43.6	394 2 Q89YX4	Q89YX4 bacteroides
52	44	43.6	402 2 Q7VX60	Q7VX60 bordetella
53	44	43.6	402 2 Q7W826	Q7W826 bordetella
54	44	43.6	402 2 Q7WLH3	Q7WLH3 bordetella
55	44	43.6	411 2 Q68A45	Q68A45 ralsstonia s
56	44	43.6	412 1 EG2B BRARE	Q05159 brachydanio
57	44	43.6	412 2 Q66HT5	Q66HT5 brachydanio
58	44	43.6	416 2 Q8XR46	Q8XR46 ralsstonia s
59	44	43.6	446 1 CRB3 SCHPO	Q10272 echinocacc
60	44	43.6	462 2 Q98T82	Q98T82 galium gall
61	44	43.6	474 1 MIG1 KLUTA	P50898 kluyveromyc
62	44	43.6	497 2 Q8WY24	Q8WY24 homo sapien
63	44	43.6	543 1 MIG1 KLUMA	P52288 kluyveromyc
64	44	43.6	739 2 Q8LVD0	Q8LVD0 foot-and-mo
65	44	43.6	771 2 Q9XHY4	Q9XHY4 oryza sativ
66	43.5	43.1	118 2 Q48377	Q48377 bacterioph
67	43.5	43.1	118 2 Q71TD1	Q71TD1 bacterioph
68	43.5	43.1	124 2 Q6D859	Q6D859 erwinia car
69	43	42.6	120 2 Q606D1	Q606D1 ixodes ric
70	43	42.6	133 2 Q836K9	Q836K9 enterococcu
71	43	42.6	147 1 HV1C HUMAN	P01744 homo sapien
72	43	42.6	201 2 Q9A2T1	Q9A2T1 caulobacter
73	43	42.6	202 2 Q95W67	Q95W67 myxine glut
74	43	42.6	258 1 HIS6 HAEIN	P44436 haemophilus
75	43	42.6	264 2 Q6FFG3	Q6FFG3 actinobact
76	43	42.6	352 2 Q8KZU4	Q8KZU4 uncultured
77	43	42.6	352 2 Q8LOC2	Q8LOC2 uncultured
78	43	42.6	381 2 Q66C32	Q66C32 yersinia ps
79	43	42.6	381 2 Q8ZFW8	Q8ZFW8 yersinia pe
80	43	42.6	434 2 Q8YFPI	Q8YFPI bruceella me
81	43	42.6	436 2 Q8ZG68	Q8ZG68 bruceella su
82	43	42.6	436 1 Y96X RHIL0	Q98P28 rhizobium l
83	43	42.6	453 2 Q8ZFT6	Q8ZFT6 streptomyce
84	43	42.6	537 2 Q9L6J3	Q9L6J3 oryza sativ
85	43	42.6	572 2 Q454Z2	Q454Z2 caenorhabdi
86	43	42.6	573 2 Q8A3Y7	Q8A3Y7 bacteroides
87	43	42.6	696 2 Q15838	Q15838 leishmania
88	43	42.6	763 1 THED CORGL	Q09Q11 c multilunc
89	43	42.6	879 2 Q6BIR4	Q6BIR4 debaryomyc
90	43	42.6	938 2 Q8K0N8	Q8K0N8 mus musculu
91	43	42.6	1071 1 MMT1 ARATH	Q14632 arabidopsis
92	43	42.6	1282 1 BMS1 HUMAN	Q14632 homo sapien
93	43	42.6	1284 2 Q6PGF5	Q6PGF5 mus musculu
94	43	42.6	1287 2 Q6ZOH0	Q6ZOH0 mus musculu
95	43	42.6	2151 1 KRPL HANTV	P23456 hantaa vir
96	43	42.6	2151 2 Q99AT5	Q99AT5 hantaa vir
97	43	42.6	2151 2 Q89913	Q89913 hantaa vir
98	43	42.6	2151 2 Q9DXJ9	Q9DXJ9 hantavirus
99	43	42.6	2151 2 Q9E127	Q9E127 hantavirus
100	43	42.6	2151 2 Q9QD48	Q9QD48 hantavirus

ALIGNMENTS

```
RESULT 1
Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Y.K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:815-819 (1997).
DR EMBL: U88067; AAB48044.1; -.
DR PIR: S19965; S19965.
DR PIR: S19967; S19967.
DR PIR: S19968; S19968.
DR PIR: S26325; S26325.
DR HSSP: P01607; 1BMV.
DR SMART: SM00406; IGV; 2.
DR PROSITE: PS50835; IG_LIKE; 2.
FT NON_TER 1
FT SEQUENCE 241 AA; 26086 MW; 02768872489C771 CRC64;
SQ
Query Match 100.0%; Score 101; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 2, 1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WINTYGEPTVADDFKG 17
Db 50 WINTYGEPTVADDFKG 66

RESULT 2
Q9JL79 PRELIMINARY; PRT; 102 AA.
AC Q9JL79;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A.CA;
RX MEDLINE=20448942; PubMed=10992488;
RX DOI=10.1128/IAI.68.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin";
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL: AF206027; AAF69325.1; -.
DR HSSP: P01751; 1NOB.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003596; IGV.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 241 AA; 26086 MW; 02768872489C771 CRC64;
```

```
FT NON_TER 102
SQ SEQUENCE 102 AA; 11543 MW; E590C292093F6711 CRC64;
Query Match 91.1%; Score 92; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 2, 6e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 WINTYGEPTVADDFKG 17
Db 35 WINTYGEPTVADDFKG 51

RESULT 3
Q683Y7 PRELIMINARY; PRT; 116 AA.
AC Q683Y7;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Immunoglobulin heavy chain variable region (Fragment).
GN Name=IGHV;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c;
RA Phalipon A., Costachel C., Thuniz A., Nato F.;
RT "Anti-lipopolysaccharide antibodies protective against Shigella
RT flexneri 2a infection recognize an immunodominant serotype-specific
RT determinant on the O-antigen.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ784033; CAH04483.1; -.
DR InterPro: IPR003599; IGV.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003596; IG_V.
DR PIR: PFO0047; IGV; 1.
DR PIR: SM00409; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 116 AA; 12863 MW; SEC1AD02E911952 CRC64;
SQ
Query Match 86.1%; Score 87; DB 2; Length 116;
Best Local Similarity 88.2%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 WINTYGEPTVADDFKG 17
Db 50 WINTYGEPTVADDFKG 66

RESULT 4
Q683Y8 PRELIMINARY; PRT; 116 AA.
AC Q683Y8;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Immunoglobulin heavy chain variable region (Fragment).
GN Name=IGHV;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c;
RA Phalipon A., Costachel C., Thuniz A., Nato F.;
RT "Anti-lipopolysaccharide antibodies protective against Shigella
RT flexneri 2a infection recognize an immunodominant serotype-specific
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 60.75 Seconds
(without alignments)
50.931 Million cell updates/sec

Title: US-10-018-245A-3
Perfect score: 51
Sequence: 1 YDYDGFDPY 8

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	8	5	AAAG80313
2	51	100.0	117	5	AAAG80317
3	44	86.3	108	6	ABU02662
4	44	86.3	108	8	ADK47752
5	44	86.3	120	8	ADR94312
6	43	84.3	120	2	AAW05825
7	43	84.3	139	2	AAW36167
8	43	84.3	139	2	AAW36165
9	43	84.3	182	6	ABU70516
10	43	84.3	279	2	AAW05826
11	43	84.3	359	4	AAE04200
12	43	84.3	359	8	ABG64502
13	43	84.3	359	8	ADL77769
14	43	84.3	363	3	AAAB36391
15	43	84.3	408	5	ABP69127
16	43	84.3	542	3	ABB36394
17	43	84.3	592	4	AAE04244
18	43	84.3	706	5	ABP69128
19	43	84.3	708	3	AAU09860
20	43	84.3	736	3	AAAB36392
21	43	84.3	736	4	AAAB93215
22	43	84.3	736	4	AAAB93142
23	43	84.3	736	4	AAAB88373
24	43	84.3	736	5	ABP69129
25	43	84.3	736	5	AAU09861

26	43	84.3	736	5	AD128041
27	43	84.3	747	3	AAAB36393
28	43	84.3	747	3	ABR63160
29	43	84.3	804	4	AAAB94482
30	43	84.3	806	5	ABG66709
31	43	84.3	806	5	ABG66686
32	42	82.4	144	2	AAAB08346
33	40.5	79.4	11	8	ADSL8692
34	40.5	79.4	11	8	ADSL8666
35	40.5	79.4	450	8	ADSL8702
36	40.5	79.4	450	8	ADSL8708
37	40	78.4	12	2	AAAB27040
38	40	78.4	121	2	AAAB53584
39	40	78.4	121	5	ABG32687
40	40	78.4	121	5	ABG32695
41	40	78.4	121	5	ABG32683
42	40	78.4	121	5	ABG32693
43	40	78.4	121	5	ABG32689
44	40	78.4	121	5	ABG32685
45	40	78.4	121	5	ABG32681
46	40	78.4	121	5	ABG32691
47	40	78.4	121	5	AAE27809
48	40	78.4	121	5	AAE27823
49	40	78.4	121	5	AAE27815
50	40	78.4	121	5	AAE27821
51	40	78.4	121	5	AAE27811
52	40	78.4	121	5	AAE27813
53	40	78.4	121	5	AAE27817
54	40	78.4	121	5	AAE27819
55	40	78.4	140	2	AAAB27049
56	40	78.4	140	2	AAAB27051
57	40	78.4	242	2	AAAB79870
58	40	78.4	242	2	AAAB79872
59	40	78.4	242	2	AAAB79871
60	40	78.4	244	2	AAAB79868
61	40	78.4	244	2	AAAB79867
62	40	78.4	244	2	AAAB79873
63	40	78.4	246	2	AAAB79869
64	40	78.4	574	6	AAAB72635
65	40	78.4	652	2	AAAB48650
66	39	76.5	120	4	AAAB13721
67	39	76.5	124	4	AAAB13825
68	39	76.5	124	4	AAAB32770
69	39	76.5	124	4	AAAB26232
70	39	76.5	124	4	AAAB27600
71	39	76.5	124	4	AAAB18253
72	39	76.5	124	4	AAAB65958
73	39	76.5	124	4	AAAB53577
74	39	76.5	124	4	ABG47622
75	39	76.5	124	5	ABG35604
76	39	76.5	161	5	ABAB77790
77	39	76.5	515	8	ADRB6925
78	39	76.5	515	8	ADRB6923
79	39	76.5	545	2	AAAY24418
80	39	76.5	545	2	AAAY24418
81	39	76.5	545	2	ABG32846
82	39	76.5	561	5	ABAB77791
83	39	76.5	561	5	ADDB82125
84	39	76.5	579	3	AAAB56837
85	39	76.5	588	7	ADCB30951
86	39	76.5	588	7	ADDB82127
87	39	76.5	623	3	AAAY70242
88	39	76.5	623	3	ABO53025
89	39	76.5	623	7	ADDB82129
90	39	76.5	623	8	ADDB82129
91	39	76.5	623	8	ADDB82129
92	39	76.5	623	8	ADDB82129
93	39	76.5	623	8	ADDB82129
94	39	76.5	623	8	ADDB82129
95	39	76.5	623	8	ADDB82129
96	39	76.5	704	4	AAAG74545
97	39	76.5	704	4	AAAG74545
98	39	76.5	704	4	AAAG74545
99	39	76.5	704	4	AAAG74545
100	39	76.5	704	4	AAAG74545

99 38 74.5 105 3 AAY77993
100 38 74.5 119 2 AAR25728

AAY77993 Amino aci
AAR25728 Humanised

ALIGNMENTS

RESULT 1
AAG80313 standard; peptide; 8 AA.

XX AAG80313;

XX 18-FEB-2002 (first entry)

XX Anti-human TNF-alpha CDR-H3 peptide.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
XX heavy chain; light chain; complementarity determining region; vasotrophic;
XX antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
XX rheumatoid arthritis; malaria; multiple sclerosis.

XX Homo sapiens.

XX WO200179298-A1.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-JP003308.

XX 19-APR-2000; 2000JP-00117394.

XX (SUNR) SUNTORY LTD.

XX Fukuda Y, Nagahira K, Nakanishi T;

XX WPI; 2002-066345/09.

XX Novel heavy and light-chain polypeptides of chimeric and humanized
XX antibodies against human tumor necrosis factor alpha for low-
XX immunogenicity treatment of TNF-related diseases such as toxic shock
XX syndrome.

XX Claim 1c; Page 26; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides
XX or their fragments of a recombinant antibody to human TNF-alpha which
XX contain complementarity determining region (CDR) sequences. The products
XX of the invention have vasotrophic, antiarthritic, neuroprotective and
XX vivo. The antibodies act by neutralising TNF-alpha in
XX associated diseases such as toxic shock syndrome, rheumatoid arthritis,
XX malaria and multiple sclerosis. The antibodies have low immunogenicity in
XX humans. This sequence represents the anti-human tumour necrosis factor-
XX alpha (TNF-alpha) heavy chain CDR1 designated CDR-H3

XX Sequence 8 AA;

Query Match 100.0%; Score 51; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYDGFY 8
|||
Db 1 YDYDGFY 8

RESULT 2
AAG80317 standard; protein; 117 AA.

XX AAG80317;

XX 18-FEB-2002 (first entry)

XX Anti-human TNF-alpha H chain CDR region.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
XX heavy chain; light chain; complementarity determining region; vasotrophic;
XX antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
XX rheumatoid arthritis; malaria; multiple sclerosis.

XX Homo sapiens.

XX WO200179298-A1.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-JP003308.

XX 19-APR-2000; 2000JP-00117394.

XX (SUNR) SUNTORY LTD.

XX Fukuda Y, Nagahira K, Nakanishi T;

XX WPI; 2002-066345/09.

XX N-PSDB; AAI69375.

XX Novel heavy and light-chain polypeptides of chimeric and humanized
XX antibodies against human tumor necrosis factor alpha for low-
XX immunogenicity treatment of TNF-related diseases such as toxic shock
XX syndrome.

XX Disclosure; Page 27-28; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides
XX or their fragments of a recombinant antibody to human TNF-alpha which
XX contain complementarity determining region (CDR) sequences. The products
XX of the invention have vasotrophic, antiarthritic, neuroprotective and
XX vivo. The antibodies act by neutralising TNF-alpha in
XX associated diseases such as toxic shock syndrome, rheumatoid arthritis,
XX malaria and multiple sclerosis. The antibodies have low immunogenicity in
XX humans. This sequence represents the anti-human tumour necrosis factor-
XX alpha (TNF-alpha) heavy chain CDR fragment described in the invention

XX Sequence 117 AA;

Query Match 100.0%; Score 51; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.8; 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYDGFY 8
|||
Db 99 YDYDGFY 106

RESULT 3
ABU02662 standard; protein; 108 AA.

XX ABU02662;

XX 23-OCT-2003 (revised)

XX 11-FEB-2003 (first entry)

XX S. pneumoniae type 4 strain protein from coding region #2241.

XX Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;
XX antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
XX gene therapy; vaccine.

XX Streptococcus pneumoniae; type 4 strain.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:57:11 ; Search time 16.125 Seconds
(without alignments)
37.035 Million cell updates/sec

Title: US-10-018-245A-3
Perfect score: 51
Sequence: 1 YDYDGFY 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	86.3	108	4	US-09-583-110-4267
2	44	86.3	120	4	US-09-107-433-2947
3	43	84.3	120	3	US-08-397-411-10
4	43	84.3	120	3	US-08-397-411-11
5	43	84.3	139	2	US-08-656-586-4
6	43	84.3	139	2	US-08-656-586-8
7	43	84.3	279	3	US-08-397-411-13
8	40	78.4	12	1	US-07-946-421-6
9	40	78.4	121	1	US-09-254-180C-7
10	40	78.4	140	1	US-07-946-421-24
11	40	78.4	140	1	US-07-946-421-28
12	40	78.4	242	2	US-08-553-497A-26
13	40	78.4	242	2	US-08-553-497A-28
14	40	78.4	244	2	US-08-553-497A-20
15	40	78.4	244	2	US-08-553-497A-22
16	40	78.4	246	2	US-08-553-497A-24
17	39	76.5	161	2	US-09-821-687-2
18	39	76.5	545	2	US-08-990-114-1
19	39	76.5	545	3	US-09-241-333-1
20	39	76.5	561	4	US-09-821-687-4
21	38	74.5	119	1	US-07-634-278-37
22	38	74.5	119	1	US-07-634-278-60
23	38	74.5	119	1	US-07-634-278-61
24	38	74.5	119	1	US-08-477-728-37
25	38	74.5	119	1	US-08-477-728-60
26	38	74.5	119	1	US-08-477-728-61
27	38	74.5	119	1	US-08-474-040-37

28	38	74.5	119	1	US-08-474-040-60	Sequence 60, Appl
29	38	74.5	119	1	US-08-474-040-61	Sequence 61, Appl
30	38	74.5	119	1	US-08-487-200-37	Sequence 37, Appl
31	38	74.5	119	1	US-08-487-200-60	Sequence 60, Appl
32	38	74.5	119	1	US-08-487-200-61	Sequence 61, Appl
33	38	74.5	119	1	US-08-484-537-37	Sequence 37, Appl
34	38	74.5	119	3	US-08-484-537-60	Sequence 60, Appl
35	38	74.5	119	3	US-08-484-537-61	Sequence 61, Appl
36	38	74.5	138	1	US-07-634-278-33	Sequence 33, Appl
37	38	74.5	138	1	US-08-477-728-33	Sequence 33, Appl
38	38	74.5	138	1	US-08-474-040-33	Sequence 33, Appl
39	38	74.5	138	1	US-08-487-200-33	Sequence 33, Appl
40	38	74.5	138	3	US-08-484-537-33	Sequence 33, Appl
41	38	74.5	329	4	US-09-270-767-6040	Sequence 4060, A
42	38	72.5	10	1	US-08-318-970B-8	Sequence 8, Appl
43	37	72.5	363	4	US-09-489-039A-7321	Sequence 7321, Ap
44	37	72.5	654	1	US-08-332-828C-2	Sequence 2, Appl
45	37	72.5	654	3	US-09-330-945-2	Sequence 15295, A
46	37	72.5	697	4	US-09-248-796A-15295	Sequence 21570, A
47	36	70.6	63	4	US-09-248-796A-21570	Sequence 21570, A
48	36	70.6	116	2	US-08-308-494A-21	Sequence 21, Appl
49	36	70.6	236	1	US-08-335-695-22	Sequence 22, Appl
50	36	70.6	257	1	US-09-338-092-18	Sequence 18, Appl
51	36	70.6	319	4	US-09-710-279-2760	Sequence 2760, Ap
52	36	70.6	443	3	US-09-134-001C-3183	Sequence 3183, Ap
53	36	70.6	571	4	US-09-543-681A-4700	Sequence 4700, Ap
54	36	70.6	607	4	US-09-570-856B-28	Sequence 28, Appl
55	36	70.6	728	4	US-09-543-681A-8132	Sequence 8132, Ap
56	35	68.6	70	4	US-09-107-532A-5874	Sequence 5874, Ap
57	35	68.6	114	4	US-09-248-796A-27842	Sequence 27842, A
58	35	68.6	260	4	US-09-270-767-43301	Sequence 43301, A
59	35	68.6	289	4	US-09-949-016-8825	Sequence 8825, Ap
60	35	68.6	341	4	US-09-107-532A-3743	Sequence 3743, Ap
61	35	68.6	350	2	US-08-484-905-65	Sequence 65, Appl
62	35	68.6	350	2	US-08-484-905-67	Sequence 67, Appl
63	35	68.6	350	3	US-08-481-985B-65	Sequence 65, Appl
64	35	68.6	350	3	US-08-481-985B-67	Sequence 67, Appl
65	35	68.6	350	3	US-08-370-476-65	Sequence 65, Appl
66	35	68.6	350	3	US-08-370-476-67	Sequence 67, Appl
67	35	68.6	361	3	US-08-652-265-22	Sequence 22, Appl
68	35	68.6	361	3	US-08-834-497A-22	Sequence 22, Appl
69	35	68.6	361	3	US-09-503-444A-22	Sequence 22, Appl
70	35	68.6	531	4	US-09-248-796A-20235	Sequence 20235, A
71	35	68.6	1060	4	US-09-419-788-19	Sequence 19, Appl
72	34.5	67.6	119	1	US-08-491-845-2	Sequence 2, Appl
73	34.5	67.6	119	1	US-08-491-845-10	Sequence 10, Appl
74	34	66.7	14	4	US-08-914-372C-16	Sequence 16, Appl
75	34	66.7	20	2	US-08-480-190-207	Sequence 207, App
76	34	66.7	20	2	US-08-488-379-207	Sequence 207, App
77	34	66.7	20	4	US-08-475-399A-207	Sequence 207, App
78	34	66.7	20	4	US-08-077-255A-207	Sequence 207, App
79	34	66.7	20	5	PCT-US93-07545-207	Sequence 207, App
80	34	66.7	58	3	US-08-812-586-5	Sequence 5, Appl
81	34	66.7	58	3	US-09-535-832A-5	Sequence 5, Appl
82	34	66.7	61	4	US-09-270-767-18509	Sequence 38509, A
83	34	66.7	61	4	US-09-270-767-53726	Sequence 53726, A
84	34	66.7	92	4	US-09-673-809-106	Sequence 106, App
85	34	66.7	105	3	US-08-812-586-1	Sequence 1, Appl
86	34	66.7	105	4	US-09-535-832A-1	Sequence 1, Appl
87	34	66.7	156	4	US-09-513-599C-4289	Sequence 4289, App
88	34	66.7	182	1	US-08-137-954-135	Sequence 135, App
89	34	66.7	182	1	US-08-137-954-137	Sequence 137, App
90	34	66.7	182	1	US-08-137-954-138	Sequence 138, App
91	34	66.7	182	1	US-08-137-954-139	Sequence 139, App
92	34	66.7	182	1	US-08-137-954-140	Sequence 140, App
93	34	66.7	182	1	US-08-137-954-141	Sequence 141, App
94	34	66.7	182	1	US-08-137-954-142	Sequence 142, App
95	34	66.7	182	1	US-08-137-954-143	Sequence 143, App
96	34	66.7	182	1	US-08-137-954-144	Sequence 144, App
97	34	66.7	182	1	US-08-137-954-145	Sequence 145, App
98	34	66.7	182	1	US-08-137-954-150	Sequence 150, App
99	34	66.7	182	1	US-08-137-954-151	Sequence 151, App
100	34	66.7	182	1	US-08-137-954-152	Sequence 152, App

ALIGNMENTS

RESULT 1
US-09-583-110-4267
Sequence 4267, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 4267
LENGTH: 108
ORGANISM: Streptococcus pneumoniae
US-09-583-110-4267

Query Match 86.3%; Score 44; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYDGFY 8
Db 99 DYDGFY 105

RESULT 2
US-09-107-433-2947
Sequence 2947, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Denise
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 2947:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1..120
SEQUENCE DESCRIPTION: SEQ ID NO: 2947:
US-09-107-433-2947

Query Match 86.3%; Score 44; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYDGFY 8
Db 111 DYDGFY 117

RESULT 3
US-08-397-411-10
Sequence 10, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Link, Brian
APPLICANT: Teo, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-10

GenCore version 5.1.6
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Run on: March 24, 2005, 08:56:15 ; Search time 46.125 Seconds
(without alignments)
57.427 Million cell updates/sec

Title: US-10-018-245A-3

Perfect score: 51

Sequence: 1 YDYDGFDPY 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*
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18: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	43	84.3	120	15	US-10-435-299-10
4	43	84.3	120	15	US-10-435-299-11
5	43	84.3	329	15	US-10-435-299-13
6	43	84.3	279	11	US-09-833-245-1251
7	43	84.3	363	13	US-10-045-815-2
8	43	84.3	446	17	US-10-822-300-136
9	43	84.3	446	17	US-10-822-300-137
10	43	84.3	446	17	US-10-822-300-138
11	43	84.3	446	17	US-10-822-300-139
12	43	84.3	446	17	US-10-822-300-140
13	43	84.3	542	13	US-10-045-815-8

14	43	84.3	708	15	US-10-257-174-25	Sequence 25, Appl
15	43	84.3	736	13	US-10-045-815-4	Sequence 4, Appl
16	43	84.3	736	15	US-10-257-174-26	Sequence 26, Appl
17	43	84.3	736	15	US-10-312-352-33	Sequence 33, Appl
18	43	84.3	747	13	US-10-045-815-6	Sequence 6, Appl
19	40	78.4	121	15	US-10-468-370-642	Sequence 642, App
20	40	78.4	121	15	US-10-468-370-644	Sequence 644, App
21	40	78.4	121	15	US-10-468-370-646	Sequence 646, App
22	40	78.4	121	15	US-10-468-370-648	Sequence 648, App
23	40	78.4	121	15	US-10-468-370-650	Sequence 650, App
24	40	78.4	121	15	US-10-468-370-652	Sequence 652, App
25	40	78.4	121	15	US-10-468-370-654	Sequence 654, App
26	40	78.4	121	15	US-10-468-370-656	Sequence 656, App
27	40	78.4	121	15	US-10-468-528-1	Sequence 1, Appl
28	40	78.4	121	15	US-10-468-528-3	Sequence 3, Appl
29	40	78.4	121	15	US-10-468-528-5	Sequence 5, Appl
30	40	78.4	121	15	US-10-468-528-7	Sequence 7, Appl
31	40	78.4	121	15	US-10-468-528-9	Sequence 9, Appl
32	40	78.4	121	15	US-10-468-528-11	Sequence 11, Appl
33	40	78.4	121	15	US-10-468-528-13	Sequence 13, Appl
34	40	78.4	121	15	US-10-468-528-15	Sequence 15, Appl
35	40	78.4	317	16	US-10-437-963-132544	Sequence 132544, A
36	39	76.5	124	9	US-09-864-761-33551	Sequence 33551, A
37	39	76.5	161	9	US-09-821-687-2	Sequence 2, Appl
38	39	76.5	545	9	US-09-978-242-1	Sequence 1, Appl
39	39	76.5	561	9	US-09-821-687-4	Sequence 4, Appl
40	39	76.5	579	9	US-09-925-300-1415	Sequence 1415, Ap
41	39	76.5	704	14	US-10-106-698-5319	Sequence 5319, Ap
42	38	74.5	93	16	US-10-437-963-111527	Sequence 111527, A
43	38	74.5	119	15	US-10-389-155-19	Sequence 19, Appl
44	38	74.5	119	15	US-10-389-155-20	Sequence 20, Appl
45	38	74.5	119	15	US-10-389-155-21	Sequence 21, Appl
46	38	74.5	119	15	US-10-389-155-22	Sequence 22, Appl
47	38	74.5	119	15	US-10-389-155-23	Sequence 23, Appl
48	38	74.5	119	15	US-10-389-155-24	Sequence 24, Appl
49	38	74.5	119	15	US-10-389-155-25	Sequence 25, Appl
50	38	74.5	119	15	US-10-389-155-26	Sequence 26, Appl
51	38	74.5	119	15	US-10-389-155-27	Sequence 27, Appl
52	38	74.5	119	15	US-10-389-155-28	Sequence 28, Appl
53	38	74.5	119	15	US-10-389-155-29	Sequence 29, Appl
54	38	74.5	119	15	US-10-389-155-30	Sequence 30, Appl
55	38	74.5	119	15	US-10-389-155-31	Sequence 31, Appl
56	37	72.5	8	10	US-09-880-748-3092	Sequence 3092, Ap
57	37	72.5	8	15	US-10-293-418-13092	Sequence 13092, Ap
58	37	72.5	14	9	US-09-252-150-63	Sequence 63, Appl
59	37	72.5	15	9	US-09-252-150-62	Sequence 62, Appl
60	37	72.5	16	9	US-09-252-150-61	Sequence 61, Appl
61	37	72.5	125	9	US-10-424-599-160605	Sequence 160605, A
62	37	72.5	125	16	US-10-437-963-132817	Sequence 132817, A
63	37	72.5	125	16	US-10-437-963-132817	Sequence 132817, A
64	37	72.5	200	16	US-10-437-963-132817	Sequence 132817, A
65	37	72.5	243	10	US-09-880-748-2102	Sequence 2102, Ap
66	37	72.5	243	15	US-10-293-418-2102	Sequence 2102, Ap
67	37	72.5	673	14	US-10-294-561-3	Sequence 3, Appl
68	37	72.5	1229	16	US-10-437-963-132817	Sequence 132817, A
69	37	72.5	1610	16	US-10-437-963-132817	Sequence 132817, A
70	36	70.6	63	11	US-09-864-408A-416	Sequence 416, App
71	36	70.6	67	15	US-10-264-049-3574	Sequence 3574, Ap
72	36	70.6	120	9	US-09-229-200A-9	Sequence 9, Appl
73	36	70.6	120	9	US-09-229-200A-19	Sequence 19, Appl
74	36	70.6	120	9	US-09-229-200A-20	Sequence 20, Appl
75	36	70.6	120	9	US-09-229-200A-21	Sequence 21, Appl
76	36	70.6	120	9	US-09-229-200A-22	Sequence 22, Appl
77	36	70.6	120	9	US-09-229-200A-23	Sequence 23, Appl
78	36	70.6	120	9	US-09-229-200A-24	Sequence 24, Appl
79	36	70.6	120	9	US-09-229-200A-25	Sequence 25, Appl
80	36	70.6	120	9	US-09-229-200A-26	Sequence 26, Appl
81	36	70.6	120	9	US-09-229-200A-27	Sequence 27, Appl
82	36	70.6	120	9	US-09-229-200A-28	Sequence 28, Appl
83	36	70.6	120	9	US-10-437-963-132817	Sequence 132817, A
84	36	70.6	120	9	US-10-437-963-132817	Sequence 132817, A
85	36	70.6	301	9	US-09-799-777-64	Sequence 64, Appl
86	36	70.6	425	15	US-10-369-493-1158	Sequence 1158, Ap

87 36 70.6 435 9 US-09-815-242-5283 Sequence 5283, Ap
88 36 70.6 436 9 US-09-815-242-12600 Sequence 12600, A
89 36 70.6 436 9 US-09-815-242-12732 Sequence 12732, A
90 36 70.6 436 15 US-10-282-122A-43793 Sequence 43793, A
91 36 70.6 436 15 US-10-282-122A-70602 Sequence 70602, A
92 36 70.6 436 15 US-10-282-122A-71683 Sequence 71683, A
93 36 70.6 436 17 US-10-857-625-660 Sequence 660, App
94 36 70.6 563 15 US-10-425-114-58931 Sequence 58931, A
95 36 70.6 570 15 US-10-425-114-62721 Sequence 62721, A
96 36 70.6 579 15 US-10-425-114-56520 Sequence 56520, A
97 36 70.6 581 15 US-10-425-114-63215 Sequence 63215, A
98 36 70.6 738 16 US-10-451-467A-238 Sequence 238, App
99 35.5 69.6 123 16 US-10-663-244-15 Sequence 15, Appl
100 35.5 69.6 123 16 US-10-663-244-97 Sequence 97, Appl

ALIGNMENTS

RESULT 1
US-10-018-245A-3
; Sequence 3, Application US/10018245A
; Publication No. US20040115196A1
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Yoshiaki
; APPLICANT: NAGAHIRA, Kazuhiro
; APPLICANT: NAKANISHI, Yoshihiro
; TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
; TITLE OF INVENTION: determining regions and genes encoding the same
; FILE REFERENCE: 46224
; CURRENT APPLICATION NUMBER: US/10/018,245A
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: JP 117394/2000
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: CDR-H3 of anti-human TNF-alpha antibody
US-10-018-245A-3
Query Match 100.0%; Score 51; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YDYDGFY 8
DB 1 YDYDGFY 8
RESULT 2
US-10-472-928-4482
; Sequence 4482, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926W0
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: Seqw199, version 1.03
; SEQ ID NO 4482
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:

; OTHER INFORMATION: hypothetical protein
; OTHER INFORMATION: Cellular location: Cytoplasm
; OTHER INFORMATION: Similar to strain R6 sequence 15903989 (8.E-63)
US-10-472-928-4482

Query Match 86.3%; Score 44; DB 17; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYDGFY 8
DB 99 DYDGFY 105

RESULT 3
US-10-435-299-10
; Sequence 10, Application US/10435299
; Publication No. US20040052783A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Teo, J. Yun
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD3
; FILE REFERENCE: 05882-0176-CNUS04
; CURRENT APPLICATION NUMBER: US/10/435,299
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 09/618,380
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 08/397,411
; PRIOR FILING DATE: 1995-03-01
; PRIOR APPLICATION NUMBER: US 07/859,583
; PRIOR FILING DATE: 1992-03-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain of Humanized M291 Ab minus signal sequence
US-10-435-299-10
Query Match 84.3%; Score 43; DB 15; Length 120;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YDYDGFY 8
DB 102 YDYDGFY 109
RESULT 4
US-10-435-299-11
; Sequence 11, Application US/10435299
; Publication No. US20040052783A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Teo, J. Yun
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD3
; FILE REFERENCE: 05882-0176-CNUS04
; CURRENT APPLICATION NUMBER: US/10/435,299
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 09/618,380
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 08/397,411
; PRIOR FILING DATE: 1995-03-01
; PRIOR APPLICATION NUMBER: US 07/859,583
; PRIOR FILING DATE: 1992-03-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1

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OM protein - protein search, using sw model

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68.421 Million cell updates/sec

Title: US-10-018-245A-3

Perfect score: 51

Sequence: 1 YDYDGFY 8

Scoring table: BLOSUM62
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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	40	78.4	1322	2	B71440
6	39	76.5	365	2	I68896
7	39	76.5	647	2	F70057
8	38	74.5	106	1	NKASTP
9	38	74.5	117	2	S17586
10	38	74.5	123	2	B30560
11	38	74.5	282	2	T35294
12	38	74.5	493	2	S78384
13	37	72.5	195	2	D84364
14	37	72.5	673	2	A49878
15	36	70.6	210	2	G97235
16	36	70.6	231	2	E90002
17	36	70.6	257	2	S50288
18	36	70.6	301	2	JM0079
19	36	70.6	321	2	A69088
20	36	70.6	391	2	I54530
21	36	70.6	425	2	F69193
22	36	70.6	436	2	C89926
23	36	70.6	540	2	T00463
24	36	70.6	559	2	A42807
25	36	70.6	560	2	T32288
26	36	70.6	607	2	S24754
27	36	70.6	738	2	S37876
28	36	70.6	752	2	H86770
29	36	70.6	1198	2	T49726

30	35	68.6	91	2	I58989	MHC H2-K transplan
31	35	68.6	91	2	I59068	MHC class I H2-K-b
32	35	68.6	109	2	S26325	Ig heavy chain V r
33	35	68.6	131	2	A27472	Ig heavy chain pre
34	35	68.6	163	2	C81283	flavodoxin Cj182c
35	35	68.6	180	2	S37891	hypothetical prote
36	35	68.6	201	2	C40040	alternative splici
37	35	68.6	201	2	S26404	H-2 class I histoc
38	35	68.6	206	2	JL0059	conserved hypothet
39	35	68.6	216	2	A64962	hypothetical prote
40	35	68.6	216	2	F85815	hypothetical prote
41	35	68.6	216	2	G90967	hypothetical prote
42	35	68.6	235	2	T47379	alternative splici
43	35	68.6	248	2	A40040	protein containing
44	35	68.6	255	2	G97227	alternative splici
45	35	68.6	292	2	B40040	conserved hypothet
46	35	68.6	319	2	H69043	conserved hypothet
47	35	68.6	323	2	T32874	hypothetical prote
48	35	68.6	328	1	S54392	npp protein - Ent
49	35	68.6	353	1	S56750	single stranded D
50	35	68.6	360	2	A27638	MHC class I histoc
51	35	68.6	361	1	HLRB	MHC class I histoc
52	35	68.6	361	2	I46858	MHC class I RLA pr
53	35	68.6	362	2	A45849	MHC class I histoc
54	35	68.6	362	2	A45876	MHC class I histoc
55	35	68.6	365	2	I57814	MHC class I-alpha
56	35	68.6	369	1	HLMSKB	MHC class I histoc
57	35	68.6	369	1	HLMSKB	MHC class I histoc
58	35	68.6	422	2	G72227	hypothetical prote
59	35	68.6	474	1	G2MS11	Ig gamma-2b chain
60	35	68.6	876	2	B90547	lipoprotein (impor
61	35	68.6	1385	2	H88569	protein K03H1.5 [i
62	35	68.6	1409	2	S41028	hypothetical prote
63	35	68.6	118	2	AB2104	hypothetical prote
64	34	66.7	137	2	I80172	class I histoccompa
65	34	66.7	137	2	I80175	class I histoccompa
66	34	66.7	137	2	I80176	class I histoccompa
67	34	66.7	137	2	I80174	class I histoccompa
68	34	66.7	181	2	I59188	MHC cell surface g
69	34	66.7	203	2	E81449	hypothetical prote
70	34	66.7	206	2	I37528	HLA-Cw1 - human (I
71	34	66.7	210	2	S73509	MHC class I HLA-J
72	34	66.7	218	2	I72808	class I-related se
73	34	66.7	241	1	HLMSPR	MHC H-2K1-k - mous
74	34	66.7	243	2	I54459	MHC HLA-A cell sur
75	34	66.7	243	2	I54412	MHC class I histoc
76	34	66.7	273	1	HLHU69	MHC class I histoc
77	34	66.7	273	2	I38509	MHC class I histoc
78	34	66.7	276	2	T52316	chlorophyll a/b-bi
79	34	66.7	305	2	S07115	class I histoccompa
80	34	66.7	308	2	I36956	MHC CHLA histoc - c
81	34	66.7	322	2	A21125	MHC class I histoc
82	34	66.7	325	2	S20045	MHC class I histoc
83	34	66.7	329	2	A40730	MHC class I histoc
84	34	66.7	338	2	A39953	MHC class I histoc
85	34	66.7	338	2	I56116	MHC HLA-B27-HS - h
86	34	66.7	339	2	I56071	MHC class I histoc
87	34	66.7	345	1	B41732	heterogeneous nucl
88	34	66.7	350	2	I54308	MHC HLA B71 - huma
89	34	66.7	350	2	I68747	MHC class I lympho
90	34	66.7	353	2	F64175	hypothetical prote
91	34	66.7	354	2	S24438	class I histoccompa
92	34	66.7	354	2	S24436	class I histoccompa
93	34	66.7	355	2	B40730	class I histoccompa
94	34	66.7	355	2	I80171	class I histoccompa
95	34	66.7	355	2	I80169	class I histoccompa
96	34	66.7	357	2	S11136	class I histoccompa
97	34	66.7	357	2	S11133	class I histoccompa
98	34	66.7	357	2	S11140	class I histoccompa
99	34	66.7	357	2	AD1062	protein kinase (im
100	34	66.7	358	2	S03538	class I histoccompa

ALIGNMENTS

RESULT 1

C95250

hypothetical protein SP2139 [imported] - Streptococcus pneumoniae (strain TIGR4)

C/Species: Streptococcus pneumoniae

C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C/Accession: C95250

C/Retcelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple, nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A./Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A/Reference number: A95000; MUID:21357209; PMID:11463916

A/Accession: C95250

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-108 <KUR>

A/Cross-references: UNIPROT:Q97NB3; GB:AE005672; PIDN:AAK76196.1; PID:G14973651; GSPDB:C

A/Experimental source: strain TIGR4

C/Genetics:

A/Gene: SP2139

Query Match

Best Local Similarity 86.3%; Score 44; DB 2; Length 108;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query

2 DYDGFY 8
|||||
Db 99 DYDGFY 105

RESULT 2

A99715

hypothetical protein spr1948 [imported] - Streptococcus pneumoniae (strain R6)

C/Species: Streptococcus pneumoniae

C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C/Accession: A99715

C/Hoskins, J.A.; Albhorn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; Ee, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A/Reference number: A97872; MUID:21429245; PMID:11544234

A/Accession: A99715

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-108 <KUR>

A/Cross-references: UNIPROT:Q8CY66; GB:AE007317; PIDN:AAI00750.1; PID:G15459647; GSPDB:C

C/Genetics:

A/Gene: spr1948

Query Match

Best Local Similarity 86.3%; Score 44; DB 2; Length 108;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query

2 DYDGFY 8
|||||
Db 99 DYDGFY 105

RESULT 3

T28269

ORF MSV108 hypothetical protein - Melanoplus sanguinipes entomopoxvirus

C/Species: Melanoplus sanguinipes entomopoxvirus

C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C/Accession: T28269

R/Afonso, C.L.; Tullman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A/Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A/Reference number: Z20484; MUID:99102612; PMID:9847359

A/Accession: T28269

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-76 <AFO>

A/Cross-references: UNIPROT:Q9YVY4; EMBL:AF063866; NID:G4049647; PIDN:AAQ97654.1; PID:G4(

C/Genetics:

A/Note: MSV108

Query Match

Best Local Similarity 82.4%; Score 42; DB 2; Length 76;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query

1 YDVGFDY 8
|||||
Db 38 YDVGFDY 45

RESULT 4

S60067

Ig heavy chain V region (monoclonal antibody C3, gamma 2A) [validated] - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 23-Feb-1996 #sequence_revision 10-Oct-1997 #text_change 23-Mar-2001

C/Accession: S60067

R/Wien, M.W.; Filman, D.J.; Stura, E.A.; Guillot, S.; Delpeyroux, F.; Crainic, R.; Hogle, Nat. Struct. Biol. 2, 232-243, 1995

A/Title: Structure of the complex between the Fab fragment of a neutralizing antibody for

A/Reference number: S60066; MUID:95292109; PMID:7539711

A/Accession: S60067

A/Molecule type: mRNA

A/Residues: 1-123 <WIE>

A/Cross-references: EMBL:X84698; NID:G773225

R/Wien, M.W.; Hogle, J.M.

submitted to the Brookhaven Protein Data Bank, January 1995

A/Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 1-123

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin; pyroglytamic acid

F/1/Modified site: pyroglutamate carboxylic acid (Gln) #status predicted

F/22-96/Diulfide bonds: #status experimental

Query Match

Best Local Similarity 79.4%; Score 40.5; DB 2; Length 123;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query

1 YDVGFDY 8
|||||
Db 101 YDVGFDY 109

RESULT 5

B71440

hypothetical protein d14605c - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

A/Variety: Columbia

C/Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004

C/Accession: B71440

R/Beran, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Hempel, S.; Kotter, F.; Eutlian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A/Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech,

erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Anic C.; Chaitzias, N.

A/Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal

A/Reference number: A71400; MUID:98121113; PMID:9461215

A/Accession: B71440

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-1322 <BEV>

A/Cross-references: UNIPROT:O23559; GB:Z97342; NID:G2245031; PID:G2245072

C/Genetics:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 52.75 Seconds
(without alignments)
77.661 Million cell updates/sec

Title: US-10-018-245A-3
Perfect score: 51
Sequence: 1 YVDYGFY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	86.3	91	2	005165 streptococc
2	44	86.3	108	2	097NB3 streptococc
3	44	86.3	108	2	08CY66 streptococc
4	44	86.3	348	2	064Q75 bacteroides
5	44	86.3	560	2	043319 artemisia a
6	44	86.3	561	2	06DFC0 xenopus lae
7	43	84.3	363	2	09HC87 homo sapien
8	43	84.3	542	2	09QZT6 mus musculu
9	43	84.3	728	2	09RIY8 mus musculu
10	43	84.3	736	2	096SK8 homo sapien
11	43	84.3	736	2	096SL5 homo sapien
12	43	84.3	736	2	09HC86 homo sapien
13	43	84.3	738	2	08BSV2 mus musculu
14	43	84.3	739	2	08CFJ3 mus musculu
15	43	84.3	742	2	09CMK5 mus musculu
16	43	84.3	747	2	09QZT7 mus musculu
17	43	84.3	765	2	06NTI9 xenopus lae
18	43	84.3	804	2	096SN3 homo sapien
19	42	82.4	76	2	09YVY4 melanoplus
20	42	82.4	772	2	08RCG0 fusobacteri
21	41	80.4	758	2	06F7M5 actinobact
22	41	80.4	1658	2	091BW3 indian citr
23	40	78.4	308	2	073S89 mycobacteri
24	40	78.4	574	2	017411 aedes aegypt
25	40	78.4	1126	2	073ME8 treponema d
26	40	78.4	1322	2	023559 arabidopsis
27	40	78.4	3320	2	073MR0 treponema d
28	39	76.5	365	2	06Z585 peromyzomys
29	39	76.5	367	2	08A1B3 bacteroides
30	39	76.5	533	1	ROQ_RAT
31	39	76.5	561	2	068ED6 mus musculu

32	39	76.5	623	1	ROQ_HUMAN	060506 homo sapien
33	39	76.5	623	1	ROQ_MOUSE	07cmx3 mus musculu
34	39	76.5	624	2	06NS22 xenopus lae	06ns22 xenopus lae
35	39	76.5	630	2	06NUZ3 brachydanio	06nu23 brachydanio
36	39	76.5	647	2	070997 bacillus su	070997 bacillus su
37	39	76.5	725	2	06UH08 gallus gall	06uh08 gallus gall
38	39	76.5	772	2	07P394 fusobacteri	07p394 fusobacteri
39	38	74.5	105	1	RNMS_ASPPSA	P06653 aspergillus
40	38	74.5	282	2	06MDT7 streptomyce	06mdt7 streptomyce
41	38	74.5	282	2	09S2Q8 streptomyce	09s2q8 streptomyce
42	38	74.5	283	2	06WDS5 euryymna sc	06wds5 euryymna sc
43	38	74.5	283	2	06WDN8 euryymna sc	06wdn8 euryymna sc
44	38	74.5	284	2	06WDN3 euryymna sc	06wdn3 euryymna sc
45	38	74.5	284	2	06WDN4 euryymna sc	06wdn4 euryymna sc
46	38	74.5	327	1	MTX1_DROME	09vth6 drosophila
47	38	74.5	340	2	08ABX9 fusobacteri	08abx9 fusobacteri
48	38	74.5	360	2	07P891 chimpanzee	07p891 chimpanzee
49	38	74.5	375	2	087448 oryza sativ	087448 oryza sativ
50	38	74.5	385	2	0650Y1 dictyosteli	0650y1 dictyosteli
51	38	74.5	435	2	06TMJ7 dictyosteli	06tmj7 dictyosteli
52	38	74.5	435	2	0861B2 dictyosteli	0861b2 dictyosteli
53	38	74.5	493	1	ACCD_EPIVI	P30064 epifagus vi
54	38	74.5	695	2	052863 sodalis glo	052863 sodalis glo
55	38	74.5	158	2	06CWX0 kluyveromyc	06cwx0 kluyveromyc
56	37	72.5	184	2	081ZD4 bacillus an	081zd4 bacillus an
57	37	72.5	189	2	061480 bacillus an	061480 bacillus an
58	37	72.5	195	1	VATE_HAINT	Q9hne0 halobacteri
59	37	72.5	260	1	TRUA_SPIKU	P60355 epiloplaama
60	37	72.5	291	2	06NU14 xenopus lae	06nu14 xenopus lae
61	37	72.5	295	2	0645K2 brachydanio	0645k2 brachydanio
62	37	72.5	296	2	07SXN2 xenopus tro	07sxn2 xenopus tro
63	37	72.5	297	2	0640N2 methanosaic	0640n2 methanosaic
64	37	72.5	305	2	08PW15 mus musculu	08pw15 mus musculu
65	37	72.5	344	2	061893 bacteroides	061893 bacteroides
66	37	72.5	350	2	064WP9 bacteroides	064wp9 bacteroides
67	37	72.5	375	2	08A8W9 bacteroides	08a8w9 bacteroides
68	37	72.5	673	2	027082 tachypleus	027082 tachypleus
69	37	72.5	742	2	06CJN7 kluyveromyc	06cjt7 kluyveromyc
70	37	72.5	931	2	06CB39 yarrowia li	06cb39 yarrowia li
71	37	72.5	1025	2	09V636 drosophila	09v636 drosophila
72	37	72.5	1040	2	09LNG0 arabidopsis	09lng0 arabidopsis
73	37	72.5	2514	2	07RD79 plasmodium	07rd79 plasmodium
74	37	72.5	4099	2	09C7Z6 arabidopsis	09c7z6 arabidopsis
75	37	72.5	4099	2	06X9Z3 equus caball	06x9z3 equus caball
76	36	70.6	105	2	09AFB6 anaerococcu	09afb6 anaerococcu
77	36	70.6	110	2	09AFB7 anaerococcu	09afb7 anaerococcu
78	36	70.6	111	2	09AFB9 anaerococcu	09afb9 anaerococcu
79	36	70.6	111	2	09AFB4 anaerococcu	09afb4 anaerococcu
80	36	70.6	181	2	07YNZ6 sus scrofa	07ynz6 sus scrofa
81	36	70.6	210	2	097FK9 clostridium	097fk9 clostridium
82	36	70.6	231	2	08NVH0 staphylococ	08nvh0 staphylococ
83	36	70.6	231	2	09VSG2 staphylococ	09vsg2 staphylococ
84	36	70.6	231	2	07A4F2 staphylococ	07a4f2 staphylococ
85	36	70.6	231	2	06G7L4 staphylococ	06g7l4 staphylococ
86	36	70.6	231	2	06GEX9 staphylococ	06gex9 staphylococ
87	36	70.6	254	2	09XYT0 rhyzopertha	09xyt0 rhyzopertha
88	36	70.6	256	2	09TPK9 monodelphis	09tpk9 monodelphis
89	36	70.6	257	1	YBE3_YEAST	P81893 saccharomyc
90	36	70.6	271	2	07XZK7 homo sapien	07xz7 homo sapien
91	36	70.6	293	2	07XZK3 xenopus lae	07xz3 xenopus lae
92	36	70.6	298	2	06SPR2 homo sapien	06spr2 homo sapien
93	36	70.6	301	2	07KZ75 mus musculu	07kz75 mus musculu
94	36	70.6	301	2	09Z130 pseudomonas	09z130 pseudomonas
95	36	70.6	308	2	088AB4 methanobact	088ab4 methanobact
96	36	70.6	321	2	027690 schistosoma	027690 schistosoma
97	36	70.6	339	2	06C142 kluyveromyc	06c142 kluyveromyc
98	36	70.6	349	2	06C142 kluyveromyc	06c142 kluyveromyc
99	36	70.6	356	1	AROB_THETN	Q6rb14 thermocanaer
100	36	70.6	356	1	AROB_THETN	Q6rb14 thermocanaer

ALIGNMENTS

RESULT 1

005165 ID 005165 PRELIMINARY; PRT; 91 AA.
AC 005165;
DT 01-JUN-1997 (TREMblrel. 04, Created)
DT 01-JUN-1997 (TREMblrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6;
RX MEDLINE=98340517; PubMed=9675866;
RA Sanchez-Beato A., Lopez R., Garcia J.;
RT "Molecular characterization of PcpA: a novel choline-binding protein
of Streptococcus pneumoniae."
RL FEMS Microbiol. Lett. 164:207-214 (1998).
DR EMBL; Z82001; CAB04757.1; -.
KM Hypothetical protein.
SQ SEQUENCE 91 AA; 11056 MW; 7CA9A5C88F33A585 CRC64;

Query Match 86.3%; Score 44; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYDGFY 8
Db 82 DYDGFY 88

RESULT 2

097NB3 ID 097NB3 PRELIMINARY; PRT; 108 AA.
AC 097NB3;
DT 01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Hypothetical protein SP2139.
GN OrderedLocustNames=SP2139.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
RA Tetteijn H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin L.A., Gwinn M.L., Kolonay J.F., Nelson M.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Kadane D.,
RA Holtzapfe E.K., Knout H.M., Wolf A.M., Uletterack T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiolini S.V., Dickinson T.,
RA Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
pneumoniae."
RL Science 293:498-506 (2001).
DR EMBL; AE007502; AAK76196.1; -.
DR PIR; C95250; C95250.
DR TIGR; SP2139; -.
KM Complete proteome; Hypothetical protein
SQ SEQUENCE 108 AA; 13150 MW; 218F51E4BDAF20A CRC64;

Query Match 86.3%; Score 44; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYDGFY 8

Db 99 DYDGFY 105

RESULT 3

08CY66 ID 08CY66 PRELIMINARY; PRT; 108 AA.
AC 08CY66;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Hypothetical protein spr1948.
GN OrderedLocustNames=spr1948;
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=171101;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21429245; PubMed=11544234;
RX DOI=10.1128/JB.183.19.5709-5717.2001;
RA Hoskins J., Alborn W.E., Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA Leblanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Nicay T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rokey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R., Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6."
RL J. Bacteriol. 183:5709-5717 (2001).
DR EMBL; AE008559; ALA00750.1; -.
DR PIR; A99715; A99715.
KM Complete proteome.
SQ SEQUENCE 108 AA; 13107 MW; 362F464ABC30DEC CRC64;

Query Match 86.3%; Score 44; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYDGFY 8
Db 99 DYDGFY 105

RESULT 4

064075 ID 064075 PRELIMINARY; PRT; 348 AA.
AC 064075;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Putative endo-beta-N-acetylglucosaminidase.
GN ORFNames=BF3613;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacterioidaceae; Bacterioides.
OX NCBI_Taxid=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
inversions regulating cell surface adaptation."
RT Proc. Natl. Acad. Sci. U.S.A. 0:0-0 (2004).
DR EMBL; AP006841; BAD50356.1; -.
DR EMBL; AP006841; BAD50356.1; -.
SQ SEQUENCE 348 AA; 39951 MW; 5ADA0761BFF73EF3 CRC64;

Query Match 86.3%; Score 44; DB 2; Length 348;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 91.125 Seconds
(without alignments)
50.931 Million cell updates/sec

Title: US-10-018-245A-4
Perfect score: 58
Sequence: 1 TASSSVSFSYLH 12

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	12	5	AAG80314 Anti-huma
2	58	100.0	108	5	AAG80318 Anti-huma
3	50	86.2	12	3	AAH10004 H. pylori
4	50	86.2	12	8	ADJ25666 Mouse apc
5	50	86.2	12	8	ADJ25666 Mouse apc
6	50	86.2	108	8	AAH10021 H. pylori
7	50	86.2	108	8	ADJ25650 Mouse act
8	50	86.2	129	8	ADJ25650 Mouse act
9	50	86.2	129	8	ADJ25650 Mouse act
10	50	86.2	129	8	ADJ25650 Mouse act
11	47	81.0	109	8	ADQ31869 Humanised
12	47	81.0	109	8	ADQ31871 Humanised
13	47	81.0	109	8	ADQ31868 Humanised
14	47	81.0	109	8	ADQ31867 Humanised
15	47	81.0	109	8	ADQ31870 Humanised
16	47	81.0	130	8	ADQ31877 Humanised
17	47	81.0	130	8	ADQ31866 Murine an
18	47	81.0	130	8	ADQ31881 Murine an
19	47	81.0	215	8	ADQ31885 Antibody
20	46	79.3	12	5	AAU70355 Mouse Kap
21	46	79.3	108	8	AAU70355 Mouse Kap
22	46	79.3	110	2	AAW46482 SICS VK a
23	46	79.3	130	2	AAW73291 R6 monocl
24	46	79.3	215	8	ADN97547 Artificial
25	46	79.3	483	8	ADN97549 Artificial

26	46	79.3	826	2	AAU30101 An acetyl
27	45	77.6	12	4	AAH81967 Ganglios
28	45	77.6	57	6	ABU56885 BONT/A Hc
29	45	77.6	108	3	AAU59306 DC8 light
30	45	77.6	109	4	AAH81974 Ganglios
31	45	77.6	109	4	AAH81971 Ganglios
32	45	77.6	110	2	AAH21307 Murine VL
33	45	77.6	110	2	AAH21306 Murine VL
34	45	77.6	110	2	AAH21287 Murine VL
35	45	77.6	131	4	AAH81976 Ganglios
36	45	77.6	195	2	AAH06477 Light cha
37	45	77.6	214	5	ABH76125 Recombina
38	45	77.6	215	2	AAH43674 Mouse ant
39	45	77.6	215	2	AAH99644 Anti-DGH
40	45	77.6	215	2	AAH97377 Murine an
41	45	77.6	225	2	AAH05710 TRX40. 9/
42	45	77.6	225	2	AAH06478 TRX40. 3/
43	45	77.6	225	2	AAH43675 Single ch
44	45	77.6	225	2	AAH99645 Single ch
45	45	77.6	236	2	AAH06479 TRX61. 3/
46	45	77.6	236	2	AAH43676 Single ch
47	45	77.6	236	2	AAH99646 Single ch
48	45	77.6	236	2	AAH02188 TRX61 sin
49	45	77.6	239	2	AAH43679 Single ch
50	45	77.6	239	2	AAH99649 Single ch
51	45	77.6	239	2	AAH02191 18-2-3/TR
52	45	77.6	241	2	AAH06482 18-2-3-/T
53	45	77.6	242	2	AAH06483 18-2-3-/T
54	45	77.6	242	2	AAH43680 Single ch
55	45	77.6	242	2	AAH99650 Single ch
56	45	77.6	242	2	AAH02192 18-2-3/TR
57	45	77.6	246	2	AAH06480 TRX59. 3/
58	45	77.6	246	2	AAH43677 Single ch
59	45	77.6	246	2	AAH99647 Single ch
60	45	77.6	246	2	AAH02189 TRX59 sin
61	45	77.6	250	2	AAH43678 Single ch
62	45	77.6	250	2	AAH99648 Single ch
63	45	77.6	250	2	AAH02190 TRX104b s
64	45	77.6	951	3	AAV44993 DC8CFV-e
65	45	77.6	44	7	ADH62642 Mouse ant
66	45	77.6	45	7	ADH62641 Mouse ant
67	45	77.6	45	7	ADH62640 Mouse ant
68	45	77.6	57	6	ABU56841 BONT/A Hc
69	45	77.6	57	6	ABU56842 BONT/A Hc
70	45	77.6	60	4	AAU49473 Propionib
71	45	77.6	60	6	ABM45992 Propionib
72	45	77.6	103	2	AAU05362 HBV spec
73	45	77.6	109	2	AAH79864 Anti-EGFR
74	45	77.6	109	2	AAH79864 Anti-EGFR
75	45	77.6	109	2	AAH79864 Anti-EGFR
76	45	77.6	109	8	ADR38687 Mouse lig
77	45	77.6	109	8	ADR38692 Mouse lig
78	45	77.6	110	2	AAH21288 Murine VL
79	45	77.6	110	2	AAH21297 Murine VL
80	45	77.6	110	2	AAH21299 Murine VL
81	45	77.6	110	2	AAH21295 Murine VL
82	45	77.6	110	2	AAH21289 Murine VL
83	45	77.6	110	2	AAH21300 Murine VL
84	45	77.6	239	2	AAU17963 Mouse scf
85	45	77.6	240	8	ADH59121 Anti-X8/8
86	45	77.6	245	2	AAW25783 Anti-T3 a
87	45	77.6	255	5	AAU72866 PS-3 sing
88	45	77.6	297	2	AAU05363 HBV spec
89	45	77.6	315	4	AAH70843 SNV-ent
90	45	77.6	503	8	AAU72874 3B10xPS-2
91	45	77.6	708	5	ADJ49669 O11-assoC
92	45	77.6	242	2	AAW53881 Firefly I
93	45	77.6	788	2	AAW53882 Anti-body-
94	45	77.6	12	8	ADH25804 Anti-alpha
95	45	77.6	12	8	ADH59661 Light cha
96	45	77.6	12	8	ADH59662 Light cha
97	45	77.6	108	8	ADH25837 Anti-alpha
98	45	77.6	108	8	ADH59675 PAM4 Vx p

99 40 69.0 108 8 ADH59680
100 40 69.0 108 8 ADH59704

ADH59680 Chimeric
ADH59704 PAM4 VK P

ALIGNMENTS

RESULT 1
AAG80314
ID AAG80314 standard; peptide; 12 AA.

AC AAG80314;

DT 18-FEB-2002 (first entry)

DE Anti-human TNF-alpha CDR-L1 peptide.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KW heavy chain; light chain; complementarity determining region; vasotropic;
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KW rheumatoid arthritis; malaria; multiple sclerosis.

OS Homo sapiens.

PN W0200179298-A1.

PD 25-OCT-2001.

PF 18-APR-2001; 2001WO-JP003308.

PR 19-APR-2000; 2000JP-00117394.

PS (SUNR) SUNTORY LTD.

PI Fukuda Y, Nagahira K, Nakanishi T;

DR WPI; 2002-066345/09.

XX Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX Claim 3a; Page 26; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotropic, antiarthritic, neuroprotective and
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
CC vivo. The antibodies are used for producing chimeric and humanised
CC antibodies that may be used for the treatment and prevention of TNF-alpha
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC human. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) light chain CDR1 designated CDR-L1

XX Sequence 12 AA;

Query Match 100.0%; Score 58; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TASSVSFSYLH 12
DB 1 TASSVSFSYLH 12

RESULT 2
ID AAG80318 standard; protein; 108 AA.
XX AAG80318;
AC AAG80318;

XX 18-FEB-2002 (first entry)

DE Anti-human TNF-alpha L chain CDR region encoding DNA.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KW heavy chain; light chain; complementarity determining region; vasotropic;
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KW rheumatoid arthritis; malaria; multiple sclerosis.

OS Homo sapiens.

PN W0200179298-A1.

PD 25-OCT-2001.

PF 18-APR-2001; 2001WO-JP003308.

PR 19-APR-2000; 2000JP-00117394.

PS (SUNR) SUNTORY LTD.

PI Fukuda Y, Nagahira K, Nakanishi T;

DR WPI; 2002-066345/09.

DR N-PSDB; AAI69376.

XX Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX Disclosure; Page 28-29; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotropic, antiarthritic, neuroprotective and
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
CC vivo. The antibodies are used for producing chimeric and humanised
CC antibodies that may be used for the treatment and prevention of TNF-alpha
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC human. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) light chain CDR fragment described in the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 58; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TASSVSFSYLH 12
DB 24 TASSVSFSYLH 35

RESULT 3
ID AAB10004 standard; protein; 12 AA.
XX AAB10004;

DT 01-NOV-2000 (first entry)

DE H. pylori 26 kDa protein-binding antibody light chain CDR1 peptide.

XX Acid-resistant microorganism; detection; faecal; intestine; infection;
KW monoclonal antibody; light chain; complementarity determining region;
KW CDR.

XX Unidentified.
OS

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:57:11 ; Search time 24.1875 Seconds
(without alignments)
37.035 Million cell updates/sec

Title: US-10-018-245A-4
Perfect score: 58
Sequence: 1 TASSSVSFSYLH 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: Issued Patents AA: *
2: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/6CTUS_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	86.2	244	1	US-08-230-843-2
2	50	86.2	244	2	US-08-636-936-2
3	46	79.3	12	4	US-09-563-222C-35
4	46	79.3	130	2	US-08-659-567-2
5	46	79.3	231	1	US-08-681-432-1
6	45	77.6	110	4	US-09-726-219A-237
7	45	77.6	214	4	US-09-653-755A-5
8	45	77.6	215	6	5455030-3
9	45	77.6	215	6	5455030-3
10	45	77.6	225	6	5455030-5
11	45	77.6	225	6	5455030-5
12	45	77.6	236	6	5455030-7
13	45	77.6	236	6	5455030-7
14	45	77.6	239	6	5455030-13
15	45	77.6	239	6	5455030-13
16	45	77.6	242	6	5455030-15
17	45	77.6	242	6	5455030-15
18	45	77.6	247	6	5455030-9
19	45	77.6	247	6	5455030-9
20	45	77.6	248	6	5455030-11
21	45	77.6	248	6	5455030-11
22	43	74.1	110	4	US-09-726-219A-256
23	43	74.1	110	4	US-09-486-814A-6
24	42	72.4	103	4	US-08-553-497A-14
25	42	72.4	109	4	US-09-233-290-7
26	42	72.4	109	4	US-09-726-219A-238
27	42	72.4	110	4	US-09-726-219A-238

28	42	72.4	110	4	US-09-726-219A-239	Sequence 239, App
29	42	72.4	110	4	US-09-726-219A-245	Sequence 245, App
30	42	72.4	110	4	US-09-726-219A-246	Sequence 246, App
31	42	72.4	110	4	US-09-726-219A-247	Sequence 247, App
32	42	72.4	110	4	US-09-726-219A-249	Sequence 249, App
33	42	72.4	110	4	US-09-726-219A-250	Sequence 250, App
34	42	72.4	110	4	US-09-726-219A-258	Sequence 258, App
35	42	72.4	110	4	US-09-486-814A-2	Sequence 2, App1
36	39	67.2	108	3	US-08-483-749A-8	Sequence 8, App1
37	38	65.5	109	3	US-08-002-324-4	Sequence 4, App1
38	38	65.5	109	5	PCT-US94-00261-4	Sequence 4, App1
39	37	63.8	111	1	US-08-432-694-2	Sequence 2, App1
40	37	63.8	111	1	US-08-432-694-4	Sequence 4, App1
41	37	63.8	111	1	US-08-432-694-14	Sequence 14, App1
42	37	63.8	106	1	US-07-634-278-1	Sequence 1, App1
43	37	63.8	106	1	US-07-634-278-7	Sequence 7, App1
44	37	63.8	106	1	US-07-634-278-8	Sequence 8, App1
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49	37	63.8	106	1	US-08-477-728-16	Sequence 16, App1
50	37	63.8	106	1	US-08-474-040-1	Sequence 1, App1
51	37	63.8	106	1	US-08-474-040-7	Sequence 7, App1
52	37	63.8	106	1	US-08-474-040-8	Sequence 8, App1
53	37	63.8	106	1	US-08-474-040-16	Sequence 16, App1
54	37	63.8	106	1	US-08-487-200-1	Sequence 1, App1
55	37	63.8	106	1	US-08-487-200-7	Sequence 7, App1
56	37	63.8	106	1	US-08-487-200-8	Sequence 8, App1
57	37	63.8	106	1	US-08-487-200-16	Sequence 16, App1
58	37	63.8	106	1	US-08-488-113B-163	Sequence 163, App
59	37	63.8	106	1	US-08-488-113B-165	Sequence 165, App
60	37	63.8	106	1	US-08-477-484B-163	Sequence 163, App
61	37	63.8	106	1	US-08-477-484B-165	Sequence 165, App
62	37	63.8	106	1	US-08-107-669D-49	Sequence 49, App1
63	37	63.8	106	1	US-08-107-669D-51	Sequence 51, App1
64	37	63.8	106	1	US-08-107-669D-83	Sequence 83, App1
65	37	63.8	106	1	US-08-472-788A-84	Sequence 84, App1
66	37	63.8	106	2	US-08-472-788A-89	Sequence 89, App1
67	37	63.8	106	2	US-08-477-531B-49	Sequence 49, App1
68	37	63.8	106	2	US-08-477-531B-51	Sequence 51, App1
69	37	63.8	106	2	US-08-646-360-163	Sequence 163, App
70	37	63.8	106	2	US-08-646-360-165	Sequence 165, App
71	37	63.8	106	2	US-08-082-842A-83	Sequence 83, App1
72	37	63.8	106	2	US-08-082-842A-84	Sequence 84, App1
73	37	63.8	106	3	US-08-934-841-2	Sequence 2, App1
74	37	63.8	106	3	US-08-839-765-163	Sequence 163, App
75	37	63.8	106	3	US-08-839-765-165	Sequence 165, App
76	37	63.8	106	3	US-09-136-389-163	Sequence 163, App
77	37	63.8	106	3	US-09-136-389-165	Sequence 165, App
78	37	63.8	106	3	US-08-484-537-1	Sequence 1, App1
79	37	63.8	106	3	US-08-484-537-7	Sequence 7, App1
80	37	63.8	106	3	US-08-484-537-16	Sequence 16, App1
81	37	63.8	106	3	US-08-484-537-163	Sequence 163, App
82	37	63.8	106	3	US-09-610-838-165	Sequence 165, App
83	37	63.8	106	3	US-09-610-838-163	Sequence 163, App
84	37	63.8	106	4	US-09-711-485-163	Sequence 163, App
85	37	63.8	106	4	US-09-711-485-165	Sequence 165, App
86	37	63.8	110	4	US-09-726-219A-248	Sequence 248, App
87	37	63.8	126	1	US-07-634-278-21	Sequence 21, App1
88	37	63.8	126	1	US-08-477-728-21	Sequence 21, App1
89	37	63.8	126	1	US-08-474-040-21	Sequence 21, App1
90	37	63.8	126	1	US-08-487-200-21	Sequence 21, App1
91	37	63.8	126	3	US-08-484-537-21	Sequence 21, App1
92	37	63.8	213	2	US-08-737-129A-8	Sequence 8, App1
93	37	63.8	239	3	US-08-279-772A-8	Sequence 8, App1
94	37	63.8	239	3	US-08-902-486-11	Sequence 11, App1
95	37	63.8	599	1	US-08-463-163-31	Sequence 31, App1
96	37	63.8	661	4	US-09-248-796A-17080	Sequence 17080, A
97	36	62.1	111	4	US-08-432-694-8	Sequence 8, App1
98	36	62.1	71	4	US-09-248-796A-27081	Sequence 27081, A
99	36	62.1	97	3	US-09-280-028-4	Sequence 4, App1
100	36	62.1	100	2	US-08-308-494A-15	Sequence 15, App1

ALIGNMENTS

RESULT 1
US-08-230-843-2
Sequence 2, Application US/08230843
Patent No. 5582826
GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: HAMURO, JUNJI
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: KANAYAMA, YUKA
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/230,843
FILING DATE: 21-APR-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 094491/1993
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 036065/1994
FILING DATE: 07-MAR-1994
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5582826man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0674-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-230-843-2

Query Match 86.2%; Score 50; DB 1; Length 244;
Best Local Similarity 91.7%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TASSSVSFSYLH 12
|||||
Db 25 TASSSVSSYLH 36

RESULT 2
US-08-636-936-2
Sequence 2, Application US/08636936
Patent No. 5856140
GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: HAMURO, JUNJI

APPLICANT: NAKAZAWA, HARUMI
APPLICANT: KANAYAMA, YUKA
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/636,936
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/230,843
FILING DATE: 21-APR-1994
APPLICATION NUMBER: JP 094491/1993
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 036065/1994
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5856140man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0674-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-636-936-2

Query Match 86.2%; Score 50; DB 2; Length 244;
Best Local Similarity 91.7%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TASSSVSFSYLH 12
|||||
Db 25 TASSSVSSYLH 36

RESULT 3
US-09-563-222C-35
Sequence 35, Application US/09563222C
Patent No. 6696620
GENERAL INFORMATION:
APPLICANT: EPICYTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HEIN, MICH B.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILE REFERENCE: 068904-0501
CURRENT APPLICATION NUMBER: US/09/563,222C
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: PCT/US01/14349
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/563,222
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 182

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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:56:15 ; Search time 69.1875 Seconds
(without alignments)
57.427 Million cell updates/sec

Title: US-10-018-245A-4
Perfect score: 58
Sequence: 1 TASSVSFSYLH 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*
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19: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	47	81.0	109	16	US-10-818-068-8
6	47	81.0	109	16	US-10-818-068-9
7	47	81.0	109	16	US-10-818-068-10
8	47	81.0	109	16	US-10-818-068-11
9	47	81.0	109	16	US-10-818-068-12
10	47	81.0	109	17	US-10-724-274-7
11	47	81.0	109	17	US-10-724-274-8
12	47	81.0	109	17	US-10-724-274-9
13	47	81.0	109	17	US-10-724-274-10

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15	47	81.0	109	17	US-10-724-274-12	Sequence 12, App1
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18	47	81.0	130	17	US-10-724-274-18	Sequence 18, App1
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21	47	81.0	215	17	US-10-822-300-141	Sequence 141, App1
22	47	81.0	215	17	US-10-724-274-26	Sequence 26, App1
23	47	81.0	215	17	US-10-724-274-32	Sequence 32, App1
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25	46	79.3	12	16	US-10-783-950-35	Sequence 35, App1
26	46	79.3	215	16	US-10-679-620-120	Sequence 120, App1
27	46	79.3	428	14	US-10-156-761-12746	Sequence 12746, A
28	46	79.3	483	16	US-10-679-620-122	Sequence 122, App
29	45	77.6	110	16	US-10-803-622-237	Sequence 237, App
30	45	77.6	110	16	US-10-803-653-237	Sequence 237, App
31	43	74.1	110	16	US-10-803-622-256	Sequence 256, App
32	43	74.1	110	16	US-10-803-622-257	Sequence 257, App
33	43	74.1	110	16	US-10-803-653-256	Sequence 256, App
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36	42	72.4	45	14	US-10-243-130-20	Sequence 20, App1
37	42	72.4	45	14	US-10-243-130-21	Sequence 21, App1
38	42	72.4	45	17	US-10-901-650-20	Sequence 20, App1
39	42	72.4	45	17	US-10-901-650-21	Sequence 21, App1
40	42	72.4	109	9	US-09-144-886-92	Sequence 92, App1
41	42	72.4	109	9	US-09-144-886-97	Sequence 97, App1
42	42	72.4	109	16	US-10-632-706-89	Sequence 89, App1
43	42	72.4	109	16	US-10-632-706-94	Sequence 94, App1
44	42	72.4	110	16	US-10-803-622-238	Sequence 238, App
45	42	72.4	110	16	US-10-803-622-239	Sequence 239, App
46	42	72.4	110	16	US-10-803-622-240	Sequence 240, App
47	42	72.4	110	16	US-10-803-622-241	Sequence 241, App
48	42	72.4	110	16	US-10-803-622-242	Sequence 242, App
49	42	72.4	110	16	US-10-803-622-243	Sequence 243, App
50	42	72.4	110	16	US-10-803-622-244	Sequence 244, App
51	42	72.4	110	16	US-10-803-622-245	Sequence 245, App
52	42	72.4	110	16	US-10-803-622-246	Sequence 246, App
53	42	72.4	110	16	US-10-803-622-247	Sequence 247, App
54	42	72.4	110	16	US-10-803-622-248	Sequence 248, App
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57	42	72.4	110	16	US-10-803-622-251	Sequence 251, App
58	42	72.4	110	16	US-10-803-622-252	Sequence 252, App
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62	42	72.4	110	16	US-10-803-622-256	Sequence 256, App
63	40	69.0	12	15	US-10-389-566-1673	Sequence 1673, App
64	40	69.0	12	17	US-10-461-888-1	Sequence 1, App1
65	40	69.0	108	15	US-10-461-888-9	Sequence 9, App1
66	40	69.0	108	15	US-10-461-888-14	Sequence 14, App1
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68	40	69.0	109	15	US-10-461-888-12	Sequence 12, App1
69	40	69.0	109	17	US-10-461-888-12	Sequence 12, App1
70	40	69.0	109	17	US-10-461-888-16	Sequence 16, App1
71	39	67.2	372	15	US-10-359-493-6709	Sequence 6709, App
72	38	65.5	57	16	US-10-437-963-177320	Sequence 177320, App
73	38	65.5	109	9	US-09-144-886-98	Sequence 98, App1
74	38	65.5	109	16	US-10-632-706-95	Sequence 95, App1
75	38	65.5	160	14	US-10-081-455-54	Sequence 54, App1
76	38	65.5	318	10	US-09-934-455-90	Sequence 90, App1
77	38	65.5	318	15	US-10-825-066A-524	Sequence 524, App
78	38	65.5	318	15	US-10-374-780A-2328	Sequence 2328, App
79	38	65.5	1204	16	US-10-437-963-188462	Sequence 188462, App
80	38	65.5	1233	16	US-10-437-963-188471	Sequence 188471, App
81	37	63.8	63	15	US-10-425-114-44700	Sequence 44700, App
82	37	63.8	83	15	US-10-468-370-647	Sequence 647, App
83	37	63.8	104	15	US-10-468-370-647	Sequence 647, App
84	37	63.8	104	15	US-10-468-370-647	Sequence 647, App
85	37	63.8	106	14	US-10-127-890-163	Sequence 163, App
86	37	63.8	106	14	US-10-127-890-165	Sequence 165, App

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87 37 63.8 106 15 US-10-340-189-83 Sequence 83, Appl
88 37 63.8 106 15 US-10-340-189-84 Sequence 84, Appl
89 37 63.8 106 15 US-10-389-155-1 Sequence 1, Appl
90 37 63.8 106 15 US-10-389-155-27 Sequence 27, Appl
91 37 63.8 106 15 US-10-389-155-28 Sequence 28, Appl
92 37 63.8 106 15 US-10-325-696-49 Sequence 49, Appl
93 37 63.8 106 15 US-10-325-696-51 Sequence 51, Appl
94 37 63.8 106 15 US-10-389-417-1 Sequence 1, Appl
95 37 63.8 106 15 US-10-389-417-27 Sequence 27, Appl
96 37 63.8 106 15 US-10-389-417-28 Sequence 28, Appl
97 37 63.8 106 15 US-10-452-357-1 Sequence 1, Appl
98 37 63.8 106 15 US-10-452-357-7 Sequence 7, Appl
99 37 63.8 106 15 US-10-452-357-8 Sequence 8, Appl
100 37 63.8 106 15 US-10-452-357-16 Sequence 16, Appl

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ALIGNMENTS

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RESULT 1
US-10-018-245A-4
; Sequence 4, Application US/10018245A
; Publication No. US2004015196A1
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Yoshiaki
; APPLICANT: NAGAHIRA, Kazuhito
; APPLICANT: NAKANISHI, Yoshihiro
; TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
; TITLE OF INVENTION: determining regions and genes encoding the same
; FILE REFERENCE: 46224
; CURRENT APPLICATION NUMBER: US/10/018,245A
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: JP 117394/2000
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: CDR-L1 of anti-human TNF-alpha antibody
US-10-018-245A-4

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Query Match      100.0%; Score 58; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TASSSVSFSTYLH 12
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Db      1 TASSSVSFSTYLH 12

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RESULT 2
US-09-842-776A-19
; Sequence 19, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; TITLE OF INVENTION: IN THE STOOL
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-23
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR1) of an
; OTHER INFORMATION: antibody light chain directed to a 26 kDa-protein
; OTHER INFORMATION: epitope
US-09-842-776A-19

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Query Match      86.2%; Score 50; DB 11; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.031;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 TASSSVSFSTYLH 12
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Db      1 TASSSVSSSTYLH 12

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RESULT 3
US-09-842-776A-54
; Sequence 54, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; TITLE OF INVENTION: IN THE STOOL
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
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Best Local Similarity 91.7%; Pred. No. 0.31;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 TASSSVSFSTYLH 12
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; Sequence 7, Application US/10818068
; Publication No. US20050002930A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: METHODS OF PRODUCTION AND USE OF ANTI-INTEGRIN ANTIBODIES FOR THE
; TITLE OF INVENTION: CONTROL OF TISSUE GRANULATION
; FILE REFERENCE: 05882.0186.NPUS01
; CURRENT APPLICATION NUMBER: US/10/818,068
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-818-068-7

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Query Match      81.0%; Score 47; DB 16; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.1;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TASSSVSFSTYLH 12
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Copyright (c) 1993 - 2005 CompuGen Ltd.

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Title: US-10-018-245A-4
Perfect score: 58
Sequence: 1 TASSSVSFSYLH 12

Scoring table: BL0SUM62
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Searched: 283416 seqs, 96216763 residues
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
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3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	45	77.6	93	2 S17642	Ig kappa chain V r
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6	45	77.6	93	2 S17623	Ig kappa chain V r
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8	45	77.6	99	2 PH1060	Ig light chain V r
9	45	77.6	130	2 B32456	Ig kappa chain pre
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11	42	72.4	93	2 S17635	Ig kappa chain V r
12	42	72.4	93	2 S17625	Ig kappa chain V r
13	42	72.4	93	2 S17636	Ig kappa chain V r
14	42	72.4	93	2 S17624	Ig kappa chain V r
15	42	72.4	93	2 S17631	Ig kappa chain V r
16	42	72.4	101	2 S29582	Ig heavy chain V r
17	42	72.4	102	2 S29586	Ig kappa chain V r
18	42	72.4	102	2 S29588	Ig kappa chain V r
19	42	72.4	102	2 S13697	Ig heavy chain V r
20	42	72.4	103	2 S13695	Ig heavy chain V r
21	42	72.4	103	2 S13698	Ig heavy chain V r
22	42	72.4	106	2 S29583	Ig kappa chain V r
23	42	72.4	108	2 PS0069	Ig kappa chain V r
24	42	72.4	109	2 PT0404	Ig light chain V r
25	42	72.4	109	2 PT0405	Ig light chain V r
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27	42	72.4	124	2 S05267	Ig kappa chain pre
28	41	70.7	108	2 PS0073	Ig kappa chain V r
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32	40	69.0	130	2 A32513	Ig kappa chain pre
33	40	69.0	331	2 F72694	hypothetical prote
34	40	69.0	572	2 S77249	hypothetical prote
35	40	69.0	770	2 T50308	probable translati
36	39	67.2	93	2 S17632	Ig kappa chain V r
37	39	67.2	372	2 T31060	hypothetical prote
38	38	65.5	93	2 S17641	Ig kappa chain V r
39	38	65.5	109	2 S13699	Ig kappa chain V r
40	38	65.5	124	2 S20633	Ig kappa chain - h
41	38	65.5	318	2 T00402	homeodomain transc
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43	37	63.8	93	2 S17634	Ig kappa chain V r
44	37	63.8	107	2 PD0011	Ig kappa chain V r
45	37	63.8	107	2 PC4405	Ig kappa chain V r
46	37	63.8	200	2 S64905	hypothetical prote
47	37	63.8	365	2 S50409	hypothetical prote
48	37	63.8	450	2 AG1370	glucose-6-phosphat
49	37	63.8	450	2 AE1740	hypothetical prote
50	37	63.8	806	2 T08932	Ig kappa chain V r
51	36	62.1	91	2 S17629	Ig kappa chain V r
52	36	62.1	91	2 S17639	Ig kappa chain V r
53	36	62.1	91	2 S17630	Ig kappa chain V r
54	36	62.1	91	2 S17637	Ig kappa chain V r
55	36	62.1	94	2 S20653	Ig heavy chain V r
56	36	62.1	94	2 S20650	Ig heavy chain V r
57	36	62.1	97	2 S26341	Ig light chain V r
58	36	62.1	97	2 PH1084	Ig light chain V r
59	36	62.1	99	2 D38601	Ig kappa chain V r
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61	36	62.1	102	2 S24214	Ig kappa chain - m
62	36	62.1	102	2 S11115	Ig kappa chain V r
63	36	62.1	103	2 S29591	Ig kappa chain V r
64	36	62.1	104	2 B49049	Ig kappa chain V r
65	36	62.1	104	2 JC6076	ant i - D - dimer monoc
66	36	62.1	106	2 PS0071	Ig kappa chain V r
67	36	62.1	106	2 S11114	Ig kappa chain V r
68	36	62.1	106	2 B54378	Ig light chain V r
69	36	62.1	106	2 PS0072	Ig kappa chain V r
70	36	62.1	106	2 S11120	Ig kappa chain V r
71	36	62.1	107	1 KYMSX4	Ig kappa chain V r
72	36	62.1	107	2 S11112	Ig kappa chain V r
73	36	62.1	107	2 S11118	Ig kappa chain V r
74	36	62.1	107	2 S11116	Ig kappa chain V r
75	36	62.1	107	2 S11113	Ig kappa chain V r
76	36	62.1	107	2 PT0401	Ig light chain V r
77	36	62.1	107	2 PT0400	Ig light chain V r
78	36	62.1	107	2 PT0395	Ig light chain V r
79	36	62.1	107	2 PT0402	Ig light chain V r
80	36	62.1	107	2 S11119	Ig kappa chain V r
81	36	62.1	107	2 S11123	Ig kappa chain V r
82	36	62.1	107	2 PT0403	Ig light chain V r
83	36	62.1	107	2 PT0398	Ig light chain V r
84	36	62.1	107	2 S11121	Ig kappa chain V r
85	36	62.1	107	2 S11117	Ig kappa chain V r
86	36	62.1	107	2 PT0399	Ig light chain V r
87	36	62.1	107	2 A30562	Ig kappa chain V r
88	36	62.1	107	2 PT0406	Ig kappa chain V r
89	36	62.1	107	2 B30562	Ig kappa chain V r
90	36	62.1	108	2 G30560	Ig kappa chain V r
91	36	62.1	130	2 JL0079	Ig kappa chain pre
92	36	62.1	140	2 PL0013	Ig kappa chain pre
93	36	62.1	173	2 A71144	hypothetical prote
94	36	62.1	1671	2 S71628	sensory transducti
95	35	60.3	76	2 A48784	Ig kappa V regions
96	35	60.3	93	2 S17640	Ig kappa chain V r
97	35	60.3	108	2 S11125	Ig kappa chain V r
98	35	60.3	130	2 S04573	Ig kappa chain pre
99	35	60.3	167	2 T14620	hypothetical prote
100	35	60.3	261	2 D90123	hypothetical prote

ALIGNMENTS

RESULT 1

PH1058
Ig light chain V region (clone 163.72) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: PH1058
R/William, D.M.; Jou, N.T.; Hill, R.D.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH1058
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-99 <TIL>
A/Cross-references: UNIPROT:Q8K1F1
A/Experimental source: B cell, strain [NZB x NZW]F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 50; DB 2; Length 99;
Best Local Similarity 91.7%; Pred. No. 0.014; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1;

Qy 1 TASSVSFSYLH 12
Db 24 TASSVSFSYLH 35

RESULT 2

KVMS7B

Ig kappa chain precursor V region (S107B) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004
C/Accession: A01943
R/Kwan, S.P.; Max, E.E.; Seidman, J.G.; Leder, P.; Scharff, M.D.
Cell 26, 57-66, 1981
A/Title: Two kappa immunoglobulin genes are expressed in the myeloma S107.
A/Reference number: A01943; MUID:82115300; PMID:6799208
A/Accession: A01943
A/Molecule type: mRNA
A/Residues: 1-129 <KMA>
A/Cross-references: UNIPROT:P01680; GB:V00780; NID:951676; PIDN:CAA24157.1; PID:951677
A/Note: the sequence was determined from the differentiated gene
C/Comment: This protein, in which there is a deletion of two amino acids at the V-J recombination kappa chain S107.
C/Genetics:
A/Intons: 17/1
C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1d C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-129/Product: Ig kappa chain V region (S107B) #status predicted <MAY>
F:38-113/Domain: immunoglobulin homology <IMM>
F:45-111/Disulfide bonds: #status predicted

Query Match 79.3%; Score 46; DB 1; Length 129;
Best Local Similarity 83.3%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1;

Qy 1 TASSVSFSYLH 12
Db 46 TASSVSFSYLH 57

RESULT 3

S20651
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C/Accession: S20651; S20647
R/Losman, M.; Faasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A/Description: Relationships among antinuclear antibodies from autoimmune MRL mice reacti

A/Reference number: S20639
A/Accession: S20651
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-86 <LOS>
A/Cross-references: EMBL:X65007; NID:952647; PIDN:CAA46140.1; PID:952648; EMBL:X65010; N
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

Query Match 77.6%; Score 45; DB 2; Length 86;
Best Local Similarity 90.9%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

Qy 2 ASSSVSFSYLH 12
Db 25 ASSSVSFSYLH 35

RESULT 4

S17642

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S17642
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A/Title: Making antibody fragments using phage display libraries.
A/Reference number: S17630; MUID:91326098; PMID:1907718
A/Accession: S17642
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-93 <CLA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 93;
Best Local Similarity 90.9%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

Qy 2 ASSSVSFSYLH 12
Db 17 ASSSVSFSYLH 27

RESULT 5

S17643

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S17643
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A/Title: Making antibody fragments using phage display libraries.
A/Reference number: S17630; MUID:91326098; PMID:1907718
A/Accession: S17643
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-93 <CLA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 93;
Best Local Similarity 90.9%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

Qy 2 ASSSVSFSYLH 12

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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 79.125 Seconds
(without alignments)
77.661 Million cell updates/sec

Title: US-10-018-245A-4
Perfect score: 58
Sequence: 1 TASSSVSFSYLH 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	79.3	129	1 KV4A MOUSE	P01680 mus musculus
2	79.3	428	1 O82CX6	O82CX6 streptomyc
3	77.6	74	2 Q8VAB9	Q8VAB9 white spot
4	77.6	114	2 Q8K1F1	Q8K1F1 mus musculus
5	72.4	101	2 Q9J178	Q9J178 mus musculus
6	69.0	131	2 O81IC3	O81IC3 mus musculus
7	69.0	331	2 Q9YD9	Q9YD9 aeropyrum p
8	69.0	572	2 P73543	P73543 synecocyst
9	69.0	770	1 E8G1 SCHPO	E8G1 schizosacch
10	67.2	423	2 Q6GYK2	Q6GYK2 caenorhabdi
11	65.5	218	2 O6Q963	O6Q963 unidentified
12	65.5	318	1 ATR4 ARATH	P92953 arabidopsis
13	65.5	442	2 O8L8R2	O8L8R2 arabidopsis
14	65.5	442	2 O9M9T4	O9M9T4 arabidopsis
15	65.5	1204	2 O615B6	O615B6 oryza sativ
16	63.8	134	2 O8VDD0	O8VDD0 mus musculus
17	63.8	189	2 O6IKM8	O6IKM8 drosophila
18	63.8	200	2 O08003	O08003 saccharomyc
19	63.8	283	2 O8WSF4	O8WSF4 drosophila
20	63.8	283	2 Q9V1P7	Q9V1P7 drosophila
21	63.8	365	1 YH27 YEAST	P28625 saccharomyc
22	63.8	450	1 G6PI LISTIN	G6PI listeria mo
23	63.8	450	1 G6PI LISTIN	G6PI listeria mo
24	63.8	450	2 O71X61	O71X61 listeria mo
25	63.8	499	2 O8XSL0	O8XSL0 listeria s
26	63.8	546	2 O7XV72	O7XV72 oryza sativ
27	63.8	684	2 Q7XV79	Q7XV79 oryza sativ
28	63.8	739	2 Q960P5	Q960P5 drosophila
29	63.8	806	2 Q9SU98	Q9SU98 arabidopsis
30	63.8	958	2 O6NNB4	O6NNB4 drosophila
31	63.8	959	2 Q7KSJ6	Q7KSJ6 drosophila

32	63.8	1052	2 Q6PCR6	Q6PCR6 brachydanio
33	63.8	1153	2 Q9VFG3	Q9VFG3 drosophila
34	62.1	107	1 KV6A MOUSE	P01675 mus musculus
35	62.1	107	1 KV6B MOUSE	P01676 mus musculus
36	62.1	107	1 KV6C MOUSE	P01677 mus musculus
37	62.1	107	1 KV6D MOUSE	P01678 mus musculus
38	62.1	107	1 KV6E MOUSE	P04940 mus musculus
39	62.1	107	1 KV6F MOUSE	P04941 mus musculus
40	62.1	107	1 KV6G MOUSE	P04942 mus musculus
41	62.1	107	1 KV6I MOUSE	P04943 mus musculus
42	62.1	107	1 KV6J MOUSE	P04944 mus musculus
43	62.1	112	2 Q8K1F0	Q8K1F0 mus musculus
44	62.1	173	2 O58102	O58102 pyrococcus
45	62.1	212	2 O8R638	O8R638 burkholderi
46	62.1	215	2 O9AWL3	O9AWL3 oryza sativ
47	62.1	269	2 Q7RBU2	Q7RBU2 plasmodium
48	62.1	330	2 Q9DSU0	Q9DSU0 aecovirus d
49	62.1	409	2 Q7XAA4	Q7XAA4 oryza sativ
50	62.1	739	2 O8L7F7	O8L7F7 arabidopsis
51	62.1	822	2 O6K2K4	O6K2K4 oryza sativ
52	62.1	834	2 O8RU34	O8RU34 oryza sativ
53	62.1	1670	2 Q23901	Q23901 dictyosteli
54	62.1	1671	2 O869S5	O869S5 dictyosteli
55	60.3	127	2 Q9N8M6	Q9N8M6 trypanosoma
56	60.3	136	2 O8LJN1	O8LJN1 oryza sativ
57	60.3	139	2 O8MOP2	O8MOP2 anopheles g
58	60.3	150	2 Q76501	Q76501 lytechinus
59	60.3	167	2 Q40281	Q40281 beta vulgar
60	60.3	220	2 O81P84	O81P84 drosophila
61	60.3	257	2 Q9RHU1	Q9RHU1 alpha prote
62	60.3	257	2 Q7CCJ3	Q7CCJ3 ethylococ
63	60.3	261	2 Q98SA2	Q98SA2 quillardia
64	60.3	289	2 O61G92	O61G92 drosophila
65	60.3	307	2 O8RLZ6	O8RLZ6 haemophilus
66	60.3	307	2 Q70U53	Q70U53 haemophilus
67	60.3	310	2 O8LJN5	O8LJN5 oryza sativ
68	60.3	315	2 O61495	O61495 oryza sativ
69	60.3	366	2 Q72UN7	Q72UN7 leptospira
70	60.3	383	2 O8C1X3	O8C1X3 mus musculus
71	60.3	394	2 O8F0B7	O8F0B7 leptospira
72	60.3	395	1 UNI_PEA	O48559 pisum sativ
73	60.3	410	2 Q6J728	Q6J728 beta vulgar
74	60.3	412	1 FNG_DROME	Q24342 drosophila
75	60.3	419	1 FNG_DROME	G151_HUMAN
76	60.3	433	2 O8SUT4	O8SUT4 streptomyce
77	60.3	436	2 Q82C67	Q82C67 anopheles g
78	60.3	508	2 Q7Q4E3	Q7Q4E3 plasmodium
79	60.3	518	2 O813Q2	O813Q2 coxiella bu
80	60.3	536	2 O81F48	O81F48 candida gla
81	60.3	587	2 O6FLR4	O6FLR4 bacteroides
82	60.3	608	2 O8A9B1	O8A9B1 beta vulgar
83	60.3	617	2 O6J740	O6J740 beta vulgar
84	60.3	625	2 O6B9X6	O6B9X6 dictyosteli
85	60.3	650	2 Q74Z59	Q74Z59 ashbya gose
86	60.3	734	2 Q7OYL6	Q7OYL6 giardia lam
87	60.3	758	2 O815F4	O815F4 plasmodium
88	60.3	758	2 O8MS15	O8MS15 plasmodium
89	60.3	812	2 O6FPC3	O6FPC3 candida gla
90	60.3	885	2 Q99SH8	Q99SH8 staphylococ
91	60.3	885	2 Q7A4G3	Q7A4G3 ethylococ
92	60.3	1041	2 Q9DPQ2	Q9DPQ2 melegrid h
93	60.3	1041	2 Q9ELF7	Q9ELF7 melegrid h
94	60.3	1130	2 O815F6	O815F6 plasmodium
95	60.3	1177	2 Q75179	Q75179 oryza sativ
96	60.3	1292	2 Q9ZGE5	Q9ZGE5 heliobacilli
97	60.3	1573	2 Q94LS7	Q94LS7 oryza sativ
98	60.3	1710	2 Q9V9H7	Q9V9H7 drosophila
99	60.3	3049	2 Q7Q5I8	Q7Q5I8 giardia lam
100	58.6	108	1 KV6K_MOUSE	P04945 mus musculus

ALIGNMENTS

```

RESULT 1
KV4A_MOUSE STANDARD; PRT; 129 AA.
ID KV4A_MOUSE
AC P01680;
DT 21-JUN-1986 (Rel. 01, Last Created)
DT 21-JUN-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region S107B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82115300; PubMed=6799208; DOI=10.1016/0092-8674(81)90033-7;
RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107.";
RL Cell 26:57-66(1981).
CC -1- MISCELLANEOUS: This protein, in which there is a deletion of two
CC amino acids at the V-J recombination site (after position 118), is
CC synthesized but not secreted in cells that express and secrete the
CC normal kappa chain S107.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; J00577; AAA38780.1; -.
DR EMBL; V00780; CAA24157.1; -.
DR PIR; A01943; KMSB7B.
DR HGSP; P01679; 2RBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 1 22
FT DOMAIN 23 129 Ig kappa chain V-IV region S107B.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 57 Complementarity-determining-1.
FT DOMAIN 58 72 Framework-2.
FT DOMAIN 73 79 Complementarity-determining-2.
FT DOMAIN 80 111 Framework-3.
FT DOMAIN 112 118 Framework-4.
FT DOMAIN 119 128 Complementarity-determining-3.
FT DISULFID 45 111 Framework-4.
FT NON_TER 129 129 By similarity.
SQ SEQUENCE 129 AA; 13833 MW; E4BB73072DC6BBA CRC64;

Query Match 79.3%; Score 46; DB 1; Length 129;
Best Local Similarity 83.3%; Pred. No. 0.57;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TASSSVSFSTYH 12
DB 46 SASSSVSSSYLH 57
:|||||
:|||||

RESULT 2
ID Q82CX6 PRELIMINARY; PRT; 428 AA.
AC Q82CX6;
DT 01-JUN-2003 (TRENBLREL. 24, Created)
DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Putative ROK-family transcriptional regulator.
DE OrderedLocusNames=SAVS212;

```

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OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osomoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005042; BAC72924.1; -.
DR InterPro; IPR000600; ROK.
DR InterPro; IPR009058; Wng_hlx_DNA_bnd.
DR Pfam; PF00480; ROK; 2.
DR PROSITE; PS01125; ROK; 1.
KW Complete proteome.
SQ SEQUENCE 428 AA; 42624 MW; E4489F17A8CBA0FA CRC64;

Query Match 79.3%; Score 46; DB 2; Length 428;
Best Local Similarity 81.8%; Pred. No. 2.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASSSVSFSTYH 12
DB 271 ASSSVASFAYLH 281
:|||||
:|||||

RESULT 3
ID Q8VAB9 PRELIMINARY; PRT; 74 AA.
AC Q8VAB9;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Wsv506 (WSSV031).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21348311; PubMed=11689662;
RX DOI=10.1128/JVI.75.23.11811-11820.2001;
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RT "Complete genome sequence of the shrimp white spot bacilliform
RT virus.";
RL J. Virol. 75:11811-11820(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597;
RA Tsai M.F., Yu H.T., Tzeng H.F., Liu J.H., Chou C.M., Huang C.J.,
RA Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
RT "Identification and characterization of a shrimp white spot syndrome
RT virus (WSSV) gene that encodes a novel chimeric polypeptide of
RT cellular-type thymidine kinase and thymidylate kinase.";
RL Virology 277:100-110(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273;
RA Chen L.L., Liu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,

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OM protein - protein search, using SW model

Run on: March 24, 2005, 08:54:17 ; Search time 60.75 Seconds
(without alignments)
50,931 Million cell updates/sec

Title: US-10-018-245A-5

Perfect score: 38

Sequence: 1 YSTSNLAS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

1: A_Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	38	100.0	8	5	AAG80315
2	38	100.0	55	6	ABU56882
3	38	100.0	55	6	ABU56871
4	38	100.0	60	6	ABU56883
5	38	100.0	92	2	AAW89175
6	38	100.0	100	2	AAW07319
7	38	100.0	100	2	AAW14487
8	38	100.0	100	2	AAW9876
9	38	100.0	102	6	ABG72734
10	38	100.0	102	6	ABG72734
11	38	100.0	105	2	AAW03182
12	38	100.0	106	4	AAE13144
13	38	100.0	106	4	AAU74418
14	38	100.0	106	6	ABJ26730
15	38	100.0	106	6	ABJ26730
16	38	100.0	106	8	ADRI5134
17	38	100.0	106	8	ADRI5137
18	38	100.0	106	8	ADRI5136
19	38	100.0	106	8	ADRI5135
20	38	100.0	107	2	AAW41401
21	38	100.0	107	2	AAW41390
22	38	100.0	107	2	AAW41390
23	38	100.0	107	2	AAW41397
24	38	100.0	107	4	AAW83167
25	38	100.0	107	4	AAW83159

26	38	100.0	107	4	AAW63987
27	38	100.0	107	6	ABR40159
28	38	100.0	107	8	ADG64762
29	38	100.0	107	8	ADRI5137
30	38	100.0	107	8	ADRI5136
31	38	100.0	108	2	AAW21294
32	38	100.0	108	2	AAW21290
33	38	100.0	108	2	AAW21290
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35	38	100.0	108	2	AAW21290
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39	38	100.0	108	2	AAW21290
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73	38	100.0	108	2	AAW21290
74	38	100.0	108	2	AAW21290
75	38	100.0	108	2	AAW21290
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89	38	100.0	108	2	AAW21290
90	38	100.0	108	2	AAW21290
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94	38	100.0	108	2	AAW21290
95	38	100.0	108	2	AAW21290
96	38	100.0	108	2	AAW21290
97	38	100.0	108	2	AAW21290
98	38	100.0	108	2	AAW21290

99 38 100.0 130 2 AAY28382
100 38 100.0 130 8 ADQ31877

AAY28382 Human chi
Adq31877 Antibody

ALIGNMENTS

RESULT 1
AAG80315

ID AAG80315 standard; peptide; 8 AA.

XX AAG80315;

XX 18-FEB-2002 (first entry)

XX Anti-human TNF-alpha CDR-L2 peptide.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KM heavy chain; light chain; complementarity determining region; vasotropic;
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KM rheumatoid arthritis; malaria; multiple sclerosis.

XX Homo sapiens.

XX WO200179298-A1.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-JP003308.

XX 19-APR-2000; 2000JP-00117394.

XX (SUNR) SUNTORY LTD.

XX Fukuda Y, Nagahira K, Nakanishi T;

XX WPI; 2002-066345/09.

XX Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX Claim 3b; Page 26; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotropic, antiarthritic, neuroprotective and
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
CC vivo. The antibodies are used for producing chimeric and humanised
CC antibodies that may be used for the treatment and prevention of TNF-alpha
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC humans. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) light chain CDR1 designated CDR-L2

XX Sequence 8 AA;

Query Match 100.0%; Score 38; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSTSNLAS 8
|||
Db 1 YSTSNLAS 8

RESULT 2
ABUS6882
ID ABUS6882 standard; protein; 55 AA.
XX
AC ABUS6882;

XX 04-APR-2003 (first entry)

XX BoNT/A Hc binding antibody scfv VL region from 265 #1.

XX Botulinum neurotoxin type A; BoNT/A; mouse; light chain variable region;
KM scfv; antibody; botulism; antibacterial; single chain antibody; VL;
XX immunoglobulin.

XX Mus sp.

XX US2002155114-A1.

XX 24-OCT-2002.

XX 31-AUG-1998; 98US-00144886.

XX 31-AUG-1998; 98US-00144886.

XX (MARK/) MARKS J D.

XX (AMER/) AMERSDORFER P.

XX Marks JD, Amersdorfer P;

XX WPI; 2003-182618/18.

XX Novel antibody that specifically binds and neutralizes botulinum
PT neurotoxin type A useful for neutralizing botulinum neurotoxin and
PT treating botulism.

XX Claim 9; Page 23; 31pp; English.

XX The invention relates to an isolated antibody that specifically binds to
CC an epitope specifically bound by an antibody expressed by a clone such as
CC clone S25, C25, C39, 1C6 and clone 1F3, where the antibody binds to and
CC neutralises botulinum neurotoxin type A (BoNT/A). Also included are a
CC polypeptide comprising BoNT/A neutralising epitope comprising an epitope
CC which is specifically bound by the antibody, where the polypeptide is not
CC a full-length botulinum neurotoxin H₃C fragment and making an anti-BoNT/A
CC antibody that neutralises BoNT/A (by contacting several antibodies with
CC an epitope specifically bound by an antibody expressed by any of the
CC novel clones and isolating an antibody that specifically binds to the
CC epitope). The antibody is useful for neutralising a BoNT/A, by contacting
CC botulinum neurotoxin type A with the antibody comprising VH CDR (heavy
CC chain variable region complementarity determining region) and with a
CC second anti-BoNT/A antibody which comprises a VH CDR, where the second
CC antibody binds to a different epitope than the first anti-BoNT/A
CC antibody. The antibody is useful in the treatment of pathologies
CC associated with botulinum neurotoxin poisoning, for rapid
CC detection/diagnosis of botulism and in the detection and/or
CC quantification of BoNT/A in a biological sample obtained from an organism
CC which is indicative of a Clostridium botulinum infection of the organism.
CC The present sequence is a light chain variable region (VL) of a single
CC chain antibody (scfv) of the invention

XX Sequence 55 AA;

Query Match 100.0%; Score 38; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSTSNLAS 8
|||
Db 48 YSTSNLAS 55

RESULT 3
ABUS6871
ID ABUS6871 standard; protein; 55 AA.
XX
AC ABUS6871;
XX
DT 04-APR-2003 (first entry)

GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: March 24, 2005, 08:57:11 ; Search time 16.125 Seconds
(without alignments)
37.035 Million cell updates/sec

Title: US-10-018-245A-5
Perfect score: 38
Sequence: 1 YSTSNLAS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	100	2	US-08-308-494A-15
2	38	100.0	105	3	US-08-434-000A-12
3	38	100.0	105	3	US-09-312-157-12
4	38	100.0	105	4	US-09-717-888-12
5	38	100.0	106	4	US-09-798-689-8
6	38	100.0	107	3	US-09-171-945-50
7	38	100.0	107	3	US-09-171-945-61
8	38	100.0	107	3	US-09-171-945-65
9	38	100.0	107	3	US-09-171-945-71
10	38	100.0	108	3	US-08-483-749A-8
11	38	100.0	108	3	US-09-171-945-9
12	38	100.0	108	4	US-09-726-219A-244
13	38	100.0	109	4	US-09-232-290-7
14	38	100.0	110	4	US-09-343-698-8
15	38	100.0	110	4	US-08-325-955-8
16	38	100.0	110	4	US-09-726-219A-237
17	38	100.0	110	4	US-09-726-219A-254
18	38	100.0	110	4	US-09-726-219A-255
19	38	100.0	110	4	US-09-726-219A-256
20	38	100.0	129	2	US-08-116-778E-2
21	38	100.0	129	2	US-08-438-562-2
22	38	100.0	129	2	US-08-483-528B-92
23	38	100.0	130	4	US-09-393-385B-111
24	38	100.0	130	4	US-09-393-385B-113
25	38	100.0	133	2	US-08-116-778E-37
26	38	100.0	133	2	US-08-438-562-37
27	38	100.0	133	2	US-08-483-528B-101

28	38	100.0	213	3	US-08-630-820-6	Sequence 6, Appl
29	38	100.0	213	4	US-09-273-453-6	Sequence 6, Appl
30	38	100.0	214	4	US-09-653-755A-5	Sequence 5, Appl
31	38	100.0	215	6	5455030-3	Patent No. 5455030
32	38	100.0	215	6	5455030-3	Patent No. 5455030
33	38	100.0	225	6	5455030-5	Patent No. 5455030
34	38	100.0	225	6	5455030-5	Patent No. 5455030
35	38	100.0	235	3	US-09-171-945-17	Sequence 11, Appl
36	38	100.0	235	3	US-09-171-945-52	Sequence 52, Appl
37	38	100.0	235	3	US-09-171-945-97	Sequence 97, Appl
38	38	100.0	235	3	US-09-171-945-99	Sequence 99, Appl
39	38	100.0	236	6	5455030-7	Patent No. 5455030
40	38	100.0	236	6	5455030-7	Patent No. 5455030
41	38	100.0	244	1	US-08-230-843-2	Sequence 2, Appl
42	38	100.0	244	1	US-08-636-936-2	Sequence 2, Appl
43	38	100.0	247	6	5455030-9	Patent No. 5455030
44	38	100.0	247	6	5455030-9	Patent No. 5455030
45	38	100.0	248	6	5455030-11	Patent No. 5455030
46	38	100.0	248	6	5455030-11	Patent No. 5455030
47	38	100.0	270	2	US-08-652-507-2	Sequence 2, Appl
48	38	100.0	281	3	US-09-423-439-44	Sequence 44, Appl
49	38	100.0	353	2	US-08-661-052-16	Sequence 16, Appl
50	38	100.0	553	3	US-09-188-082-16	Sequence 16, Appl
51	38	100.0	553	3	US-09-364-088-16	Sequence 16, Appl
52	38	100.0	553	3	US-09-102-716-16	Sequence 16, Appl
53	38	100.0	666	3	US-09-423-439-51	Sequence 51, Appl
54	38	100.0	666	3	US-08-308-494A-11	Sequence 11, Appl
55	35	92.1	27	3	US-08-783-853A-55	Sequence 55, Appl
56	35	92.1	27	3	US-09-344-050-35	Sequence 35, Appl
57	35	92.1	93	3	US-08-783-853A-35	Sequence 35, Appl
58	35	92.1	93	3	US-08-783-853A-66	Sequence 66, Appl
59	35	92.1	93	3	US-09-344-050-35	Sequence 35, Appl
60	35	92.1	97	2	US-09-344-050-66	Sequence 66, Appl
61	35	92.1	97	2	US-08-308-494A-11	Sequence 11, Appl
62	35	92.1	97	3	US-09-280-028-4	Sequence 4, Appl
63	35	92.1	105	1	US-08-211-202-110	Sequence 110, Appl
64	35	92.1	105	1	US-08-459-310-4	Sequence 4, Appl
65	35	92.1	105	4	US-09-091-071-1	Sequence 1, Appl
66	35	92.1	106	1	US-07-634-278-1	Sequence 1, Appl
67	35	92.1	106	1	US-07-634-278-7	Sequence 7, Appl
68	35	92.1	106	1	US-07-634-278-8	Sequence 8, Appl
69	35	92.1	106	1	US-07-634-278-16	Sequence 16, Appl
70	35	92.1	106	1	US-08-477-728-7	Sequence 7, Appl
71	35	92.1	106	1	US-08-477-728-16	Sequence 16, Appl
72	35	92.1	106	1	US-08-477-728-16	Sequence 16, Appl
73	35	92.1	106	1	US-08-474-040-1	Sequence 1, Appl
74	35	92.1	106	1	US-08-474-040-7	Sequence 7, Appl
75	35	92.1	106	1	US-08-474-040-8	Sequence 8, Appl
76	35	92.1	106	1	US-08-474-040-16	Sequence 16, Appl
77	35	92.1	106	1	US-08-487-200-1	Sequence 1, Appl
78	35	92.1	106	1	US-08-487-200-7	Sequence 7, Appl
79	35	92.1	106	1	US-08-487-200-16	Sequence 16, Appl
80	35	92.1	106	1	US-08-487-200-8	Sequence 8, Appl
81	35	92.1	106	1	US-08-488-113B-163	Sequence 163, Appl
82	35	92.1	106	1	US-08-488-113B-164	Sequence 164, Appl
83	35	92.1	106	1	US-08-488-113B-165	Sequence 165, Appl
84	35	92.1	106	1	US-08-477-848B-163	Sequence 163, Appl
85	35	92.1	106	1	US-08-477-848B-164	Sequence 164, Appl
86	35	92.1	106	1	US-08-477-848B-165	Sequence 165, Appl
87	35	92.1	106	1	US-08-477-848B-165	Sequence 165, Appl
88	35	92.1	106	1	US-08-107-669D-50	Sequence 50, Appl
89	35	92.1	106	1	US-08-107-669D-51	Sequence 51, Appl
90	35	92.1	106	1	US-08-472-788A-50	Sequence 50, Appl
91	35	92.1	106	1	US-08-472-788A-83	Sequence 83, Appl
92	35	92.1	106	1	US-08-472-788A-84	Sequence 84, Appl
93	35	92.1	106	2	US-08-477-531B-49	Sequence 49, Appl
94	35	92.1	106	2	US-08-477-531B-50	Sequence 50, Appl
95	35	92.1	106	2	US-08-477-531B-51	Sequence 51, Appl
96	35	92.1	106	2	US-08-646-360-163	Sequence 163, Appl
97	35	92.1	106	2	US-08-646-360-164	Sequence 164, Appl
98	35	92.1	106	2	US-08-646-360-165	Sequence 165, Appl
99	35	92.1	106	2	US-08-646-360-165	Sequence 165, Appl
100	35	92.1	106	2	US-08-082-842A-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-08-308-494A-15
Sequence 15, Application US/08308494A
Patent No. 5959083
GENERAL INFORMATION:
APPLICANT: Bossett, Klaus
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Tetraivalent Bispecific Receptors, The
TITLE OF INVENTION: Preparation and Use Thereof
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,494A
FILING DATE: 21-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,739
FILING DATE: 01-JUN-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4118120.4
FILING DATE: 03-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kulik, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 05552-1186-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-494A-15

Query Match 100.0%; Score 38; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSTSNIAS 8
| | | | | | | |
Db 45 YSTSNIAS 52

RESULT 2
US-08-434-000A-12
Sequence 12, Application US/08434000A
Patent No. 6046037
GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application 1
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/367,395
FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-3510
TELEX: SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: DESCRIPTION: Guy's 13 Kappa
US-08-434-000A-12

Query Match 100.0%; Score 38; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSTSNIAS 8
| | | | | | | |
Db 48 YSTSNIAS 55

RESULT 3
US-09-312-157-12
Sequence 12, Application US/09312157
Patent No. 630341
GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 11.25 seconds
(without alignments)
68.421 Million cell updates/sec

Title: US-10-018-245a-5
Perfect score: 38
Sequence: 1 YSTSNILAS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

1: PIR_79:.*
2: PIR1:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	91	2	SI7630
2	38	100.0	91	2	SI7632
3	38	100.0	93	2	SI7642
4	38	100.0	93	2	SI7641
5	38	100.0	93	2	SI7640
6	38	100.0	93	2	SI7623
7	38	100.0	96	2	C33730
8	38	100.0	99	2	PH1059
9	38	100.0	99	2	PH1050
10	38	100.0	99	2	PH1058
11	38	100.0	130	2	A32513
12	38	100.0	140	2	PU0013
13	35	92.1	86	2	S20651
14	35	92.1	107	2	A42848
15	34	89.5	67	2	S24216
16	34	89.5	68	2	S26474
17	34	89.5	86	2	S20649
18	34	89.5	86	2	S26459
19	34	89.5	86	2	S29587
20	34	89.5	102	2	S29584
21	34	89.5	104	2	S29592
22	34	89.5	104	2	S26475
23	34	89.5	108	2	S11125
24	34	89.5	108	2	S29581
25	34	89.5	130	2	B32456
26	34	89.5	130	2	S04573
27	33	86.8	90	2	S26339
28	33	86.8	93	2	SI7633
29	33	86.8	93	2	SI7632

30	33	86.8	93	2	SI7635	Ig kappa chain v r
31	33	86.8	93	2	SI7643	Ig kappa chain v r
32	33	86.8	93	2	SI7634	Ig kappa chain v r
33	33	86.8	93	2	SI7636	Ig kappa chain v r
34	33	86.8	93	2	SI7624	Ig kappa chain v r
35	33	86.8	93	2	SI7631	Ig kappa chain v r
36	33	86.8	94	2	S26340	Ig kappa chain v r
37	33	86.8	101	2	SI3696	Ig heavy chain v r
38	33	86.8	102	2	S29582	Ig kappa chain v r
39	33	86.8	102	2	S29588	Ig kappa chain v r
40	33	86.8	102	2	SI3697	Ig heavy chain v r
41	33	86.8	103	2	SI3695	Ig kappa chain v r
42	33	86.8	103	2	SI3698	Ig heavy chain v r
43	33	86.8	105	2	S26338	Ig kappa chain v r
44	33	86.8	106	2	S29583	Ig kappa chain v r
45	33	86.8	108	2	PI0278	Ig kappa chain v r
46	33	86.8	108	2	PI0277	Ig kappa chain v r
47	33	86.8	108	2	PI0276	Ig kappa chain v r
48	33	86.8	108	2	PS0069	Ig kappa chain v r
49	33	86.8	109	2	SI3699	Ig kappa chain v r
50	33	86.8	120	2	S66536	Ig light chain v r
51	33	86.8	123	2	S05269	Ig kappa chain pre
52	33	86.8	124	2	S05267	Ig kappa chain pre
53	32	84.2	94	2	S20653	Ig heavy chain v r
54	32	84.2	94	2	S20650	Ig heavy chain v r
55	32	84.2	106	2	B54378	Ig light chain v r
56	32	84.2	107	2	SI1122	Ig kappa chain v r
57	32	84.2	108	2	S38720	Ig light chain v r
58	32	84.2	113	2	S03410	Ig kappa chain pre
59	32	84.2	129	2	D32513	Ig kappa chain pre
60	32	84.2	1356	2	S51389	ROM2 protein - yea
61	31	81.6	99	2	D38601	Ig kappa chain v r
62	31	81.6	103	2	S73440	hypothetical prote
63	31	81.6	109	2	PT0404	Ig light chain v r
64	31	81.6	109	2	PT0405	Ig light chain v r
65	31	81.6	265	2	AH3513	channel protein vi
66	31	81.6	753	2	S35371	finger protein neu
67	31	81.6	1107	2	S61667	probable membrane
68	30	78.9	138	2	T06173	photosystem II 10X
69	30	78.9	436	2	T22253	hypothetical prote
70	30	78.9	597	2	B82881	hypothetical prote
71	30	78.9	604	2	C85069	hypothetical prote
72	30	78.9	750	2	T42614	probable envelope
73	30	78.9	982	2	A97210	beta galactosidase
74	30	78.9	1466	2	G84516	probable retrolem
75	29	76.3	97	2	PH1085	Ig light chain v r
76	29	76.3	184	2	T28333	ORF MSV172 hypothe
77	29	76.3	198	2	C97638	hypothetical prote
78	29	76.3	198	2	AD2861	hypothetical prote
79	29	76.3	247	2	S66972	probable membrane
80	29	76.3	388	2	S59860	hypothetical prote
81	29	76.3	687	2	S39828	hypothetical prote
82	29	76.3	726	2	T40790	probable permease
83	29	76.3	943	2	JE0121	hypothetical 107.4
84	29	76.3	1046	2	S61610	HFW1 protein - yea
85	29	76.3	1806	2	T23298	hypothetical prote
86	28	73.7	91	2	SI7627	Ig kappa chain v r
87	28	73.7	91	2	SI7629	Ig kappa chain v r
88	28	73.7	91	2	SI7638	Ig kappa chain v r
89	28	73.7	91	2	SI7639	Ig kappa chain v r
90	28	73.7	91	2	SI7628	Ig kappa chain v r
91	28	73.7	91	2	SI7637	Ig kappa chain v r
92	28	73.7	95	2	D33730	Ig kappa chain v r
93	28	73.7	97	2	S26341	Ig light chain v r
94	28	73.7	97	2	PH1084	Ig light chain v r
95	28	73.7	98	2	S26342	Ig kappa chain v r
96	28	73.7	100	2	S29590	Ig kappa chain v r
97	28	73.7	100	2	H33730	Ig kappa chain v r
98	28	73.7	102	2	SI1115	Ig kappa chain v r
99	28	73.7	103	2	S29591	Ig kappa chain v r
100	28	73.7	104	2	JC6076	anti-D-dimer monoc

ALIGNMENTS

RESULT 1

S17630
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17630
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; PMID:91326098; PMID:1907718
A:Accession: S17630
A:Status: Preliminary
A:Molecule type: nucleic acid
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
|||
Db 40 YSTSNLAS 47

RESULT 2

S17626
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17626
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; PMID:91326098; PMID:1907718
A:Accession: S17626
A:Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-91 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
|||
Db 40 YSTSNLAS 47

RESULT 3

S17642
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17642
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; PMID:91326098; PMID:1907718
A:Accession: S17642
A:Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
|||
Db 42 YSTSNLAS 49

RESULT 4

S17641
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17641
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; PMID:91326098; PMID:1907718
A:Accession: S17641
A:Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
|||
Db 42 YSTSNLAS 49

RESULT 5

S17640
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17640
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; PMID:91326098; PMID:1907718
A:Accession: S17640
A:Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
|||
Db 42 YSTSNLAS 49

RESULT 6

S17623
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17623
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991

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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 52.75 Seconds
(without alignments)
77.661 Million cell updates/sec

Title: US-10-018-245a-5
Perfect score: 38
Sequence: 1 YSTSNLAS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : UnlProt_03:*
1: unlprot_sprot:*
2: unlprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	ID	Description
1	38	100.0	112 2	Q8K1F2 mus musculus
2	38	100.0	114 2	Q8K1F1 mus musculus
3	38	100.0	131 2	Q8K1C3 mus musculus
4	35	92.1	97 2	Q9J176 mus musculus
5	35	92.1	253 2	Q8K1C4 plasmodium
6	34	89.5	106 2	Q9U410 schistosoma
7	34	89.5	108 1	KV6K_MOUSE
8	33	86.8	101 2	Q9J178 mus musculus
9	33	86.8	112 2	Q8K1F3 mus musculus
10	32	84.2	940 2	Q6CS17 Kluveromyc
11	32	84.2	1048 2	Q9LBQ9 arthrobacte
12	32	84.2	1051 2	P70745 arthrobacte
13	32	84.2	1266 2	Q6BHVO debaryomyc
14	32	84.2	1356 1	ROM2_YEAST
15	31	81.6	32 2	Q77UT0 lactate deh
16	31	81.6	32 2	Q9JDP6 lactate deh
17	31	81.6	103 1	YA40_MYCPN
18	31	81.6	265 2	Q8YDZ0 mycoplasma
19	31	81.6	388 2	Q9K1S6 bruceella me
20	31	81.6	391 2	Q9RXP5 bruceella su
21	31	81.6	391 2	Q8FXK6 bruceella su
22	31	81.6	554 2	Q6G1X9 bartonella
23	31	81.6	595 2	Q37901 bacterioph
24	31	81.6	798 2	Q6BV08 debaryomyc
25	31	81.6	849 2	Q6DB45 erwina car
26	31	81.6	1107 2	Q12271 ascaromyce
27	31	81.6	2646 2	Q6XHA6 dictyosteli
28	30	78.9	111 2	Q8L1U6 mus musculu
29	30	78.9	138 1	FSBR_HORVU
30	30	78.9	157 2	Q9M5E0 medicago vul
31	30	78.9	170 2	Q8S311 medicago sa

32	30	78.9	247	2	Q7V7G5	Q7V7G5 prochloroco
33	30	78.9	325	2	Q9U2Z3	Q9U2Z3 caenorhabdi
34	30	78.9	345	2	Q72FW8	Q72FW8 desulfovibr
35	30	78.9	358	2	Q9P5N1	Q9P5N1 schizosacch
36	30	78.9	375	2	Q94HY4	Q94HY4 oryza sativ
37	30	78.9	375	2	Q7XC54	Q7XC54 oryza sativ
38	30	78.9	379	2	Q7SGV9	Q7SGV9 neurospora
39	30	78.9	420	2	Q20441	Q20441 caenorhabdi
40	30	78.9	431	2	Q6R8B5	Q6R8B5 sodalis glo
41	30	78.9	452	2	Q7V9S4	Q7V9S4 prochloroco
42	30	78.9	479	2	Q7RNF5	Q7RNF5 plasmodium
43	30	78.9	553	2	Q7UER7	Q7UER7 rhodospirill
44	30	78.9	567	2	Q93Q59	Q93Q59 azotobacter
45	30	78.9	597	2	Q9PPX0	Q9PPX0 ureaplasma
46	30	78.9	604	2	Q9S9W0	Q9S9W0 arabidopsis
47	30	78.9	607	2	Q9MAN8	Q9MAN8 arabidopsis
48	30	78.9	624	2	Q9FZ14	Q9FZ14 bacterioph
49	30	78.9	691	2	Q7PZH5	Q7PZH5 anopheles g
50	30	78.9	693	2	Q8BVZ1	Q8BVZ1 arbidopsis
51	30	78.9	698	2	Q8RBJ5	Q8RBJ5 thermoaer
52	30	78.9	703	2	Q8V0L3	Q8V0L3 equid herpe
53	30	78.9	726	2	Q8V0L4	Q8V0L4 equid herpe
54	30	78.9	732	2	Q7XVH8	Q7XVH8 oryza sativ
55	30	78.9	737	2	Q6YU42	Q6YU42 oryza sativ
56	30	78.9	750	2	Q39307	Q39307 equid herpe
57	30	78.9	779	2	Q8V0L2	Q8V0L2 equid herpe
58	30	78.9	804	2	Q8V0L1	Q8V0L1 equid herpe
59	30	78.9	825	2	Q8V0L0	Q8V0L0 equid herpe
60	30	78.9	921	2	Q93FE3	Q93FE3 cowdria rum
61	30	78.9	982	2	Q97G55	Q97G55 clostridium
62	30	78.9	1063	2	Q8X1B9	Q8X1B9 utillago ma
63	30	78.9	1139	2	Q83BN5	Q83BN5 coxiella bu
64	30	78.9	1466	2	Q9Z0Q3	Q9Z0Q3 arabidopsis
65	30	78.9	3869	2	Q86PQ3	Q86PQ3 cryptospori
66	29	76.3	37	2	Q7QW07	Q7QW07 giardia lam
67	29	76.3	106	2	Q9J1X6	Q9J1X6 sulfolobus
68	29	76.3	128	2	Q7VE67	Q7VE67 prochloroco
69	29	76.3	133	2	Q66MD6	Q66MD6 hepaticis c
70	29	76.3	150	2	Q88W03	Q88W03 lactobacill
71	29	76.3	156	2	Q13536	Q13536 homo sapien
72	29	76.3	173	2	Q7M9K3	Q7M9K3 wolinnella s
73	29	76.3	184	2	Q9YV50	Q9YV50 melanoplus
74	29	76.3	198	2	Q8UD11	Q8UD11 agrobacteri
75	29	76.3	218	2	Q6MTG5	Q6MTG5 mycoplasma
76	29	76.3	230	2	Q891L0	Q891L0 clostridium
77	29	76.3	247	2	Q08500	Q08500 ascaromyce
78	29	76.3	291	2	Q720X1	Q720X1 listeria mo
79	29	76.3	301	2	Q6D4Q9	Q6D4Q9 erwina car
80	29	76.3	303	2	Q86196	Q86196 pectobacter
81	29	76.3	324	2	Q7Q752	Q7Q752 giardia lam
82	29	76.3	337	2	Q677U4	Q677U4 lymphocyeti
83	29	76.3	345	2	Q87920	Q87920 yersinia in
84	29	76.3	356	2	Q7R882	Q7R882 plasmodium
85	29	76.3	388	2	Q56006	Q56006 sulfolobus
86	29	76.3	405	2	Q6M1V6	Q6M1V6 rhodospirill
87	29	76.3	407	2	Q7UEW9	Q7UEW9 streptococc
88	29	76.3	434	2	Q9ETV8	Q9ETV8 streptococc
89	29	76.3	434	2	Q9EU98	Q9EU98 streptococc
90	29	76.3	434	2	Q9F9X2	Q9F9X2 streptococc
91	29	76.3	434	2	Q8E2P6	Q8E2P6 streptococc
92	29	76.3	434	2	Q8E7W4	Q8E7W4 streptococc
93	29	76.3	449	2	Q7S912	Q7S912 neurospora
94	29	76.3	460	2	Q6E612	Q6E612 nosema locu
95	29	76.3	530	2	Q6Z211	Q6Z211 actinoplan
96	29	76.3	605	2	Q88N87	Q88N87 pseudomonas
97	29	76.3	620	2	Q8LLE0	Q8LLE0 solanum tub
98	29	76.3	635	2	Q8A114	Q8A114 bacteroides
99	29	76.3	638	2	Q9XYD8	Q9XYD8 hirtudo medi
100	29	76.3	640	2	Q8T0M4	Q8T0M4 drosophila

ALIGNMENTS

RESULT 1
 08K1F2 PRELIMINARY; PRT; 112 AA.
 AC 08K1F2;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Pianque S., Karle S., Nishiyama Y., Paul S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF516283; AAM64201.1; -.
 DR PIR; H33932; H33932.
 DR HSSP; P01837; 25C8.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 112
 SQ SEQUENCE 112 AA; 11953 MW; 4716B87FAD8543ED CRC64;

Query Match 100.0%; Score 38; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNTLAS 8
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 Db 48 YSTSNTLAS 55

RESULT 2
 08K1F1 PRELIMINARY; PRT; 114 AA.
 AC 08K1F1;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Pianque S., Karle S., Nishiyama Y., Paul S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF516284; AAM64202.1; -.
 DR PIR; A33933; A33933.
 DR PIR; PH1058; PH1058.
 DR HSSP; P01837; 25C8.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 114
 SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3EEFD1 CRC64;

Query Match 100.0%; Score 38; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNTLAS 8
 |||||

Db 50 YSTSNTLAS 57
 RESULT 3
 081IC3 PRELIMINARY; PRT; 131 AA.
 AC 081IC3;
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Immunoglobulin gamma-3 kappa chain precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MRL/MpJ-Ipr/Ipr; TISSUE=Spleen;
 RX MEDLINE=93156722; PubMed=8429833; DOI=10.1016/0161-5890(93)90089-T;
 RA Takahashi S., Itoh U., Nose M., Ono M., Yamamoto T., Kyogoku M.;
 RT "Cloning and cDNA sequence analysis of nephritic monoclonal
 antibodies derived from an MRL/Ipr lupus mouse."
 RL Mol. Immunol. 30:177-182(1993).
 DR EMBL; D14629; BAA03482.1; -.
 DR HSSP; P01679; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW signal.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 >131 Immunoglobulin gamma-3 kappa chain.
 FT NON_TER 131 131
 SQ SEQUENCE 131 AA; 14083 MW; 5E8365695466B9E CRC64;

Query Match 100.0%; Score 38; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNTLAS 8
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 Db 72 YSTSNTLAS 79

RESULT 4
 09JL76 PRELIMINARY; PRT; 97 AA.
 AC 09JL76;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Anti-myosin immunoglobulin light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2;
 RX MEDLINE=2046942; PubMed=10992488;
 RX DOI=10.1128/JAI.68.10.5803-5808.2000;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin."
 RL Infect. Immun. 68:5803-5808(2000).
 DR EMBL; AF206030; AAF69328.1; -.
 DR HSSP; P01679; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 68.3438 Seconds
(without alignments)
50.931 Million cell updates/sec

Title: US-10-018-245A-6
Perfect score: 52
Sequence: 1 HOYLRSFYT 9

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	9	5	AAG80316 Anti-huma
2	52	100.0	108	5	AAG80318 Anti-huma
3	43	82.7	170	4	AAB88442 Human mem
4	42	80.8	109	8	ADQ31869 Humanised
5	42	80.8	109	8	ADQ31871 Humanised
6	42	80.8	109	8	ADQ31868 Humanised
7	42	80.8	109	8	ADQ31867 Humanised
8	42	80.8	109	8	ADQ31870 Humanised
9	42	80.8	130	8	ADQ31877 Antibody
10	42	80.8	130	8	ADQ31866 Murine an
11	42	80.8	130	8	ADQ31881 Antibody
12	42	80.8	215	8	ADQ31885 Antibody
13	42	80.8	215	8	ADQ31891 Antibody
14	42	80.8	311	4	AAE03721 Murine ch
15	42	80.8	333	4	AAE03723 Murine ma
16	42	80.8	333	4	AAE03720 Murine ch
17	42	80.8	345	4	AAE03732 Murine ch
18	42	80.8	360	4	AAE03723 Rat chord
19	42	80.8	382	4	AAE03722 Rat chord
20	42	80.8	521	6	ADA19155 Rat astro
21	41	78.8	108	3	AAV55591 light cha
22	41	78.8	108	8	ADJ25650 Mouse act
23	41	78.8	129	8	ADJ94357 Antibody
24	40	76.9	112	6	ABJ19266 Anti-huma
25	40	76.9	282	6	ABJ19276 Anti-huma

26	39	75.0	186	8	ADG22610 Cyanophag
27	38	73.1	460	8	ADN24892 Bacterial
28	38	73.1	466	8	ADN22132 Bacterial
29	37	71.2	96	7	ADG42391 SSP doma
30	37	71.2	110	2	AAW46482 SICS VK a
31	37	71.2	215	8	ADN97547 Artilficia
32	37	71.2	244	2	AAR60780 Fv (GP-2)
33	37	71.2	415	8	ADH22302 ORF2 prot
34	37	71.2	418	7	ADG42373 Chlamydia
35	37	71.2	483	8	ADN97549 Artilficia
36	37	71.2	1136	8	ADN21456 Bacterial
37	37	71.2	1163	8	ADR86509 Aspergill
38	36.5	70.2	388	5	AAG68199 Ty1B rela
39	36.5	70.2	388	8	ADN80120 Streptomy
40	36.5	70.2	388	8	ADN97636 S fradiiae
41	36.5	70.2	390	5	AAG68200 Ty1B rela
42	36	69.2	54	4	AAW81216 Human hae
43	36	69.2	156	4	AAG65963 Human hep
44	36	69.2	214	4	AAW99905 Human exc
45	36	69.2	214	4	AAW43704 Human bla
46	36	69.2	214	8	ADF71663 Human bla
47	36	69.2	331	5	AAW50383 Human hep
48	36	69.2	439	4	AAU07423 Human hep
49	36	69.2	470	5	AAE18328 Human hep
50	36	69.2	480	4	AAV97634 Human hep
51	36	69.2	480	4	AAU07418 Human hep
52	36	69.2	480	4	AAW85217 Hepatarnas
53	36	69.2	492	4	AAW84664 Amino aci
54	36	69.2	528	5	AAE18327 Human hep
55	36	69.2	534	4	AAW85216 Hepatarnas
56	36	69.2	534	5	ABP69310 Human pol
57	36	69.2	534	5	AAW50337 Human pre
58	36	69.2	538	5	AAV97633 Human hep
59	36	69.2	582	5	AAE18326 Human hep
60	36	69.2	592	4	AAV97632 Human hep
61	36	69.2	592	4	AAW81062 Human hep
62	36	69.2	592	4	AAU07424 Human hep
63	36	69.2	592	4	AAW85215 Hepatarnas
64	36	69.2	783	8	ADJ25397 Bacterial
65	36	69.2	783	8	ADJ26154 Bacterial
66	36	69.2	783	8	ADJ25671 Bacterial
67	36	69.2	783	8	ADJ22353 Bacterial
68	35	67.3	9	3	AAW10006 H. pylori
69	35	67.3	108	3	AAW10021 H. pylori
70	35	67.3	109	8	ADP03715 Human ant
71	35	67.3	210	3	AAW60307 Arabidops
72	35	67.3	211	3	AAW04495 Arabidops
73	35	67.3	211	3	AAW24847 Arabidops
74	35	67.3	245	3	AAW60306 Arabidops
75	35	67.3	246	3	AAW24846 Arabidops
76	35	67.3	246	3	AAW04494 Arabidops
77	35	67.3	271	3	AAW60305 Arabidops
78	35	67.3	272	3	AAW04493 Arabidops
79	35	67.3	273	3	AAW24845 Arabidops
80	35	67.3	281	8	ADP03813 Human ant
81	35	67.3	310	7	ABO61617 Klebsiell
82	35	67.3	486	6	ABU30698 Protein e
83	35	67.3	506	2	AAW83126 PreTIRK48
84	35	67.3	568	4	AAW99343 RNA virus
85	35	67.3	742	2	AAW47232 Cytoomegal
86	35	67.3	899	3	AAW18285 P. gingiv
87	35	67.3	1732	2	AAW96029 P. gingiv
88	35	67.3	1732	2	AAW24787 P. gingiv
89	35	67.3	1732	2	AAW69487 Haemagglu
90	34	65.4	9	8	ADH55663 Light cha
91	34	65.4	9	8	ADH55684 Light cha
92	34	65.4	49	4	ABW64277 Dirosophi
93	34	65.4	50	4	AAW31159 Peptide #
94	34	65.4	108	7	ADH05266 Female mo
95	34	65.4	108	8	ADH59675 PM4 VK p
96	34	65.4	108	8	ADH59680 Chimeric
97	34	65.4	108	8	ADH59704 PM4 VK p
98	34	65.4	108	8	ADH80357 Murine ho

99 34 65.4 109 8 ADH59678 CPAM4 VK
100 34 65.4 109 8 ADH59710 hPAM4 VH

ALIGNMENTS

RESULT 1
AAG80316
ID AAG80316 standard; peptide; 9 AA.

XX
AC AAG80316;

XX
DT 18-FEB-2002 (first entry)

XX
DE Anti-human TNF-alpha CDR-L3 peptide.

XX
KW TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KW heavy chain; light chain; complementarity determining region; vasotropic;
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KW rheumatoid arthritis; malaria; multiple sclerosis.

XX
OS Homo sapiens.

XX
PN W0200179298-A1.

XX
PD 25-OCT-2001.

XX
PF 18-APR-2001; 2001WO-JP003308.

XX
PR 19-APR-2000; 2000JP-00117394.

XX
PA (SUNR) SUNTORY LTD.

XX
PI Fukuda Y, Nagahira K, Nakanishi T;

XX
XX WPI; 2002-066345/09.

XX
PT Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX
PS Claim 3c; Page 27; 36pp; Japanese.

XX
CC This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotropic, antiarthritic, neuroprotective and
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
CC vivo. The antibodies are used for producing chimeric and humanised
CC antibodies that may be used for the treatment and prevention of TNF-alpha
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC humans. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) light chain CDR1 designated CDR-L3

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLRSPT 9
Db 1 HOYLRSPT 9

RESULT 2
AAG80318
ID AAG80318 standard; protein; 108 AA.
XX
AC AAG80318;

XX
DT 18-FEB-2002 (first entry)

XX
DE Anti-human TNF-alpha L chain CDR region encoding DNA.

XX
KW TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KW heavy chain; light chain; complementarity determining region; vasotropic;
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KW rheumatoid arthritis; malaria; multiple sclerosis.

XX
OS Homo sapiens.

XX
PN W0200179298-A1.

XX
PD 25-OCT-2001.

XX
PF 18-APR-2001; 2001WO-JP003308.

XX
PR 19-APR-2000; 2000JP-00117394.

XX
PA (SUNR) SUNTORY LTD.

XX
PI Fukuda Y, Nagahira K, Nakanishi T;

XX
XX WPI; 2002-066345/09.

XX
DR N-PSDB; AAI69376.

XX
PT Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX
PS Disclosure; Page 28-29; 36pp; Japanese.

XX
CC This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotropic, antiarthritic, neuroprotective and
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
CC vivo. The antibodies are used for producing chimeric and humanised
CC antibodies that may be used for the treatment and prevention of TNF-alpha
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC humans. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) light chain CDR fragment described in the invention

XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 52; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLRSPT 9
Db 90 HOYLRSPT 98

RESULT 3
AAB88442
ID AAB88442 standard; protein; 170 AA.

XX
AC AAB88442;

XX
DT 23-MAY-2001 (first entry)

XX
DE Human membrane or secretory protein clone PSEC0224.

XX
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes.

XX
OS Homo sapiens.

XX
PN EPI067182-A2.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:57:11 ; Search time 18.1406 Seconds
(without alignments)
37.035 Million cell updates/sec

Title: US-10-018-245A-6

Perfect score: 52

Sequence: 1 HQYLRSPYR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	71.2	231	1	US-08-681-432-1
2	37	71.2	244	1	US-08-230-843-2
3	37	71.2	244	2	US-08-636-936-2
4	35	67.3	310	4	US-09-489-039A-8134
5	35	67.3	1732	2	US-08-570-311-10
6	35	67.3	1732	2	US-08-353-485-10
7	35	67.3	1732	4	US-09-066-330-11
8	34	65.4	55	4	US-09-270-767-34677
9	34	65.4	55	4	US-09-270-767-49894
10	34	65.4	114	4	US-09-248-796A-23592
11	34	65.4	213	3	US-09-540-236-2378
12	34	65.4	278	3	US-09-134-001C-3651
13	34	65.4	367	2	US-08-655-704B-17
14	34	65.4	367	3	US-09-107-755-17
15	34	65.4	605	3	US-09-253-991A-25512
16	34	65.4	660	4	US-09-198-452A-578
17	34	65.4	947	4	US-09-377-850-3
18	34	65.4	966	4	US-09-438-185A-541
19	33	63.5	20	4	US-09-690-454-120
20	33	63.5	92	2	US-08-273-146-45
21	33	63.5	92	2	US-08-273-146-53
22	33	63.5	134	3	US-09-540-236-3720
23	33	63.5	175	4	US-09-096-244-2
24	33	63.5	175	4	US-09-710-279-1874
25	33	63.5	188	4	US-09-248-796A-21795
26	33	63.5	195	4	US-09-173-300-42
27	33	63.5	195	4	US-10-027-450-42

28	33	63.5	217	4	US-09-690-454-112	Sequence 112, App
29	33	63.5	276	4	US-09-719-402A-6	Sequence 6, Appli
30	33	63.5	323	4	US-09-902-540-15597	Sequence 15597, A
31	33	63.5	391	4	US-09-543-681A-5945	Sequence 5945, Ap
32	33	63.5	428	4	US-09-173-300-36	Sequence 36, Appl
33	33	63.5	428	4	US-10-027-450-36	Sequence 36, Appl
34	33	63.5	443	4	US-09-173-300-38	Sequence 38, Appl
35	33	63.5	443	4	US-10-027-450-38	Sequence 38, Appl
36	33	63.5	539	4	US-09-719-402A-2	Sequence 2, Appli
37	33	63.5	738	4	US-09-252-991A-27291	Sequence 27291, A
38	33	63.5	922	4	US-09-345-236B-89	Sequence 89, Appl
39	33	63.5	1335	3	US-09-134-001C-3716	Sequence 3716, Ap
40	33	63.5	3472	2	US-08-477-451-4	Sequence 4, Appli
41	32.5	62.5	3472	4	US-09-408-020-4	Sequence 4, Appli
42	32	61.5	128	4	US-09-225-322B-10	Sequence 19, Appl
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46	32	61.5	139	4	US-09-472-087-16	Sequence 16, Appl
47	32	61.5	139	4	US-09-472-087-90	Sequence 90, Appl
48	32	61.5	146	4	US-09-472-087-21	Sequence 21, Appl
49	32	61.5	146	4	US-09-472-087-83	Sequence 93, Appl
50	32	61.5	173	4	US-09-248-796A-16376	Sequence 16376, A
51	32	61.5	174	4	US-09-893-737-188	Sequence 188, App
52	32	61.5	211	4	US-09-248-796A-16284	Sequence 16284, A
53	32	61.5	240	4	US-09-583-110-5302	Sequence 5302, Ap
54	32	61.5	244	4	US-09-107-433-1131	Sequence 1131, Ap
55	32	61.5	285	4	US-09-107-532A-6602	Sequence 6602, Ap
56	32	61.5	305	2	US-08-602-359A-42	Sequence 42, Appl
57	31	59.6	9	3	US-08-599-226-13	Sequence 13, Appl
58	31	59.6	9	3	US-09-125-098-13	Sequence 13, Appl
59	31	59.6	9	4	US-09-540-038-13	Sequence 13, Appl
60	31	59.6	69	4	US-09-583-110-3686	Sequence 3686, Ap
61	31	59.6	74	4	US-09-107-433-4683	Sequence 4683, Ap
62	31	59.6	88	4	US-09-543-681A-4318	Sequence 4318, Ap
63	31	59.6	107	1	US-08-276-852-87	Sequence 87, Appl
64	31	59.6	107	1	US-08-899-575-87	Sequence 87, Appl
65	31	59.6	107	5	US-08-899-575-87	Sequence 87, Appl
66	31	59.6	107	5	PCT-US95-08743-87	Sequence 87, Appl
67	31	59.6	109	3	US-09-025-769B-16	Sequence 16, Appl
68	31	59.6	109	4	US-09-490-070A-16	Sequence 16, Appl
69	31	59.6	109	4	US-09-490-153-16	Sequence 16, Appl
70	31	59.6	109	4	US-09-490-324-16	Sequence 16, Appl
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73	31	59.6	112	1	US-08-478-039-88	Sequence 88, Appl
74	31	59.6	112	1	US-08-476-349A-88	Sequence 88, Appl
75	31	59.6	112	4	US-09-902-540-13241	Sequence 13241, A
76	31	59.6	131	4	US-09-902-540-15267	Sequence 15267, A
77	31	59.6	149	4	US-09-732-210-1506	Sequence 1506, Ap
78	31	59.6	188	4	US-09-252-991A-22379	Sequence 22379, A
79	31	59.6	196	2	US-08-078-311-13	Sequence 13, Appl
80	31	59.6	196	2	US-08-460-402-13	Sequence 13, Appl
81	31	59.6	203	4	US-09-252-991A-21301	Sequence 21301, A
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83	31	59.6	233	2	US-08-990-818-2	Sequence 2, Appli
84	31	59.6	239	4	US-10-092-246-32	Sequence 32, Appl
85	31	59.6	239	4	US-10-092-246A-32	Sequence 32, Appl
86	31	59.6	240	4	US-10-092-246-34	Sequence 34, Appl
87	31	59.6	240	4	US-10-092-246-35	Sequence 35, Appl
88	31	59.6	257	4	US-10-092-246-2	Sequence 2, Appli
89	31	59.6	257	4	US-10-096-246A-2	Sequence 2, Appli
90	31	59.6	309	4	US-09-540-236-2027	Sequence 2027, Ap
91	31	59.6	382	2	US-08-078-311-3	Sequence 3, Appli
92	31	59.6	382	2	US-08-460-402-3	Sequence 3, Appli
93	31	59.6	405	2	US-09-248-796A-15148	Sequence 15148, A
94	31	59.6	448	2	US-08-078-311-12	Sequence 12, Appl
95	31	59.6	448	2	US-08-460-402-12	Sequence 12, Appl
96	31	59.6	482	5	US-08-184-327A-8	Sequence 8, Appli
97	31	59.6	482	5	PCT-US95-06670-8	Sequence 8, Appli
98	31	59.6	493	2	US-08-078-311-7	Sequence 7, Appli
99	31	59.6	493	2	US-08-460-402-7	Sequence 7, Appli
100	31	59.6	518	3	US-09-113-309-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-08-681-432-1
Sequence 1, Application US/08681432
Patent No. 5800991
GENERAL INFORMATION:
APPLICANT: HALEY, Boyd E.
APPLICANT: KOHLER, Heinz
APPLICANT: RAJAGOPALAN, Krishnan
APPLICANT: PAVLINKOVA, Gabriela
TITLE OF INVENTION: NUCLEOTIDE OR NUCLEOSIDE PHOTOAFFINITY
TITLE OF INVENTION: COMPOUND MODIFIED ANTIBODIES, METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND USE THEREOF AS DIAGNOSTICS AND
TITLE OF INVENTION: THERAPEUTICS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURN, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,432
FILING DATE: 23-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,822
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 028750-132
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-681-432-1

Query Match 71.2%; Score 37; DB 1; Length 231;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HOYLRSPYT 9
Db 90 HOYHRSPLT 98

RESULT 2

US-08-230-843-2
Sequence 2, Application US/08230843
Patent No. 5582826
GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: HAMURO, JUNJI
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: KANAYAMA, YUKA
APPLICANT: SUGAMURA, KAZUO

APPLICANT: TAKESHITA, TOSHIKAZU
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/230,843
FILING DATE: 21-APR-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 094491/1993
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 036065/1994
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5582826man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0674-0X
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-230-843-2

Query Match 71.2%; Score 37; DB 1; Length 244;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HOYLRSPYT 9
Db 91 HOYHRSPLT 99

RESULT 3

US-08-636-936-2
Sequence 2, Application US/08636936
Patent No. 5856140
GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: HAMURO, JUNJI
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: KANAYAMA, YUKA
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:56:15 ; Search time 51.8906 Seconds
(without alignments)
57.427 Million cell updates/sec

Title: US-10-018-245A-6
Perfect score: 52
Sequence: 1 HOYLRSPYR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppa/PCR_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubppa/PCRUS_PUBCOMB.pep:*
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- 7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep:*
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- 18: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
- 19: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	52	100.0	9	16 US-10-018-245A-6	Sequence 6, Appl1
2	42	80.8	109	16 US-10-818-068-7	Sequence 7, Appl1
3	42	80.8	109	16 US-10-818-068-8	Sequence 8, Appl1
4	42	80.8	109	16 US-10-818-068-9	Sequence 9, Appl1
5	42	80.8	109	16 US-10-818-068-10	Sequence 10, Appl1
6	42	80.8	109	16 US-10-818-068-11	Sequence 11, Appl1
7	42	80.8	109	16 US-10-818-068-12	Sequence 12, Appl1
8	42	80.8	109	17 US-10-724-274-7	Sequence 7, Appl1
9	42	80.8	109	17 US-10-724-274-8	Sequence 8, Appl1
10	42	80.8	109	17 US-10-724-274-9	Sequence 9, Appl1
11	42	80.8	109	17 US-10-724-274-10	Sequence 10, Appl1
12	42	80.8	109	17 US-10-724-274-11	Sequence 11, Appl1
13	42	80.8	109	17 US-10-724-274-12	Sequence 12, Appl1

14	42	80.8	130	16 US-10-818-068-18	Sequence 18, Appl1
15	42	80.8	130	16 US-10-818-068-22	Sequence 22, Appl1
16	42	80.8	130	16 US-10-724-274-18	Sequence 22, Appl1
17	42	80.8	130	17 US-10-724-274-22	Sequence 22, Appl1
18	42	80.8	215	16 US-10-818-068-26	Sequence 26, Appl1
19	42	80.8	215	16 US-10-822-300-141	Sequence 141, Appl1
20	42	80.8	215	17 US-10-724-274-32	Sequence 32, Appl1
21	42	80.8	215	17 US-10-724-274-32	Sequence 32, Appl1
22	39	75.0	95	15 US-10-424-559-181354	Sequence 181354, Appl1
23	38	73.1	309	9 US-09-801-368-290	Sequence 290, Appl1
24	38	73.1	460	15 US-10-369-493-7545	Sequence 7545, Appl1
25	38	73.1	466	15 US-10-369-493-4785	Sequence 4785, Appl1
26	37	71.2	96	15 US-10-301-533-33	Sequence 33, Appl1
27	37	71.2	215	16 US-10-679-620-120	Sequence 120, Appl1
28	37	71.2	291	16 US-10-437-963-202261	Sequence 202261, Appl1
29	37	71.2	415	15 US-10-346-198-92	Sequence 92, Appl1
30	37	71.2	418	15 US-10-301-533-14	Sequence 14, Appl1
31	37	71.2	428	16 US-10-437-963-18704	Sequence 187004, Appl1
32	37	71.2	463	16 US-10-679-620-122	Sequence 122, Appl1
33	37	71.2	554	16 US-10-437-963-187026	Sequence 187026, Appl1
34	37	71.2	588	14 US-10-156-763-11538	Sequence 11538, Appl1
35	37	71.2	709	16 US-10-437-963-186982	Sequence 186982, Appl1
36	37	71.2	1136	15 US-10-369-493-4109	Sequence 4109, Appl1
37	37	71.2	1936	16 US-10-437-963-204266	Sequence 204266, Appl1
38	37	71.2	2008	16 US-10-437-963-186776	Sequence 186776, Appl1
39	36.5	70.2	388	15 US-10-257-549-13	Sequence 13, Appl1
40	36.5	70.2	390	15 US-10-257-549-14	Sequence 14, Appl1
41	36	69.2	54	9 US-09-796-692-1580	Sequence 1580, Appl1
42	36	69.2	54	14 US-10-040-862-1580	Sequence 1580, Appl1
43	36	69.2	54	15 US-10-057-4758-1580	Sequence 1580, Appl1
44	36	69.2	54	15 US-10-154-884B-1580	Sequence 1580, Appl1
45	36	69.2	54	16 US-10-764-324-1580	Sequence 1580, Appl1
46	36	69.2	214	14 US-10-080-254-98	Sequence 98, Appl1
47	36	69.2	214	15 US-10-242-355-642	Sequence 642, Appl1
48	36	69.2	439	9 US-09-978-249-12	Sequence 12, Appl1
49	36	69.2	480	9 US-09-978-249-7	Sequence 7, Appl1
50	36	69.2	480	14 US-10-177-245A-6	Sequence 6, Appl1
51	36	69.2	492	16 US-10-168-795A-2	Sequence 2, Appl1
52	36	69.2	534	9 US-09-836-461-2	Sequence 2, Appl1
53	36	69.2	534	9 US-09-880-262-2	Sequence 2, Appl1
54	36	69.2	534	14 US-10-177-245A-4	Sequence 4, Appl1
55	36	69.2	534	16 US-10-258-461-2	Sequence 2, Appl1
56	36	69.2	592	9 US-09-978-249-13	Sequence 13, Appl1
57	36	69.2	592	14 US-10-177-245A-2	Sequence 2, Appl1
58	36	69.2	783	15 US-10-369-493-11386	Sequence 11386, Appl1
59	36	69.2	783	15 US-10-369-493-14430	Sequence 14430, Appl1
60	36	69.2	783	15 US-10-369-493-14704	Sequence 14704, Appl1
61	36	69.2	783	15 US-10-369-493-15187	Sequence 15187, Appl1
62	36	69.2	2005	16 US-10-437-963-171493	Sequence 171493, Appl1
63	35	67.3	9	11 US-09-842-776A-21	Sequence 21, Appl1
64	35	67.3	47	16 US-10-437-963-103159	Sequence 103159, Appl1
65	35	67.3	108	11 US-09-842-776A-54	Sequence 54, Appl1
66	35	67.3	154	15 US-10-335-977-6524	Sequence 6524, Appl1
67	35	67.3	210	16 US-10-437-963-115560	Sequence 115560, Appl1
68	35	67.3	486	15 US-10-282-122A-58622	Sequence 58622, Appl1
69	35	67.3	486	15 US-10-335-977-6526	Sequence 6526, Appl1
70	35	67.3	509	15 US-10-387-977-101	Sequence 101, Appl1
71	35	67.3	1732	14 US-10-229-066-11	Sequence 11, Appl1
72	34	65.4	9	15 US-10-461-878-3	Sequence 3, Appl1
73	34	65.4	9	17 US-10-461-885-3	Sequence 3, Appl1
74	34	65.4	50	9 US-09-864-761-48732	Sequence 48732, Appl1
75	34	65.4	108	15 US-10-461-878-9	Sequence 9, Appl1
76	34	65.4	108	15 US-10-461-878-14	Sequence 14, Appl1
77	34	65.4	108	15 US-10-461-885-9	Sequence 9, Appl1
78	34	65.4	109	15 US-10-461-878-12	Sequence 12, Appl1
79	34	65.4	109	17 US-10-461-885-11	Sequence 11, Appl1
80	34	65.4	109	17 US-10-461-885-16	Sequence 16, Appl1
81	34	65.4	159	17 US-10-644-277-8	Sequence 8, Appl1
82	34	65.4	223	9 US-09-864-761-36198	Sequence 36198, Appl1
83	34	65.4	225	15 US-10-409-938-17	Sequence 17, Appl1
84	34	65.4	229	16 US-10-437-963-125614	Sequence 125614, Appl1
85	34	65.4	220	15 US-10-425-114-59927	Sequence 59927, Appl1
86	34	65.4	296	15 US-10-425-114-64864	Sequence 64864, Appl1

87	34	65.4	330	10	US-09-746-783-82	Sequence 82, Appl
88	34	65.4	401	16	US-10-437-963-202845	Sequence 202845,
89	34	65.4	525	16	US-10-408-765A-2364	Sequence 2364, Ap
90	34	65.4	528	16	US-10-408-765A-113	Sequence 113, App
91	34	65.4	660	15	US-10-289-762-578	Sequence 578, App
92	34	65.4	812	15	US-10-104-047-2027	Sequence 2027, Ap
93	34	65.4	838	17	US-10-741-849-7233	Sequence 7233, Ap
94	34	65.4	854	15	US-10-170-385-59	Sequence 59, Appl
95	34	65.4	1087	15	US-10-369-493-6801	Sequence 6801, Ap
96	34	65.4	1564	9	US-09-801-368-244	Sequence 244, App
97	34	65.4	1564	15	US-10-369-493-22424	Sequence 22424, A
98	33	63.5	9	9	US-09-861-294-10	Sequence 10, Appl
99	33	63.5	9	9	US-09-924-099-5	Sequence 5, Appl
100	33	63.5	9	14	US-10-367-506-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-018-245a-6
; Sequence 6, Application US/10018245A
; Publication No. US2004015196A1
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Yoshiaki
; APPLICANT: NAGAHIRA, Kazuhiro
; APPLICANT: NAKAMISHI, Toshihiro
; TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
; TITLE OF INVENTION: determining regions and genes encoding the same
; FILE REFERENCE: 46224
; CURRENT APPLICATION NUMBER: US/10/018,245A
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: JP 117394/2000
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: CDR-L3 of anti-human TNF-alpha antibody
US-10-018-245a-6

Query Match
Best Local Similarity 100.0%; Score 52; DB 16; Length 9;
Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9
DB 1 HOYLRSPYT 9

RESULT 2
US-10-818-068-7
; Sequence 7, Application US/10818068
; Publication No. US20050002930A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: METHODS OF PRODUCTION AND USE OF ANTI-INTEGRIN ANTIBODIES FOR THE
; TITLE OF INVENTION: CONTROL OF TISSUE GRANULATION
; FILE REFERENCE: 05882.0186.NPUS01
; CURRENT APPLICATION NUMBER: US/10/818,068
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-818-068-7

Query Match 80.8%; Score 42; DB 16; Length 109;

Best Local Similarity 88.9%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9
DB 90 HOYLRSPYT 98

RESULT 3
US-10-818-068-8
; Sequence 8, Application US/10818068
; Publication No. US20050002930A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: METHODS OF PRODUCTION AND USE OF ANTI-INTEGRIN ANTIBODIES FOR THE
; TITLE OF INVENTION: CONTROL OF TISSUE GRANULATION
; FILE REFERENCE: 05882.0186.NPUS01
; CURRENT APPLICATION NUMBER: US/10/818,068
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-818-068-8

Query Match 80.8%; Score 42; DB 16; Length 109;
Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9
DB 90 HOYLRSPYT 98

RESULT 4
US-10-818-068-9
; Sequence 9, Application US/10818068
; Publication No. US20050002930A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: METHODS OF PRODUCTION AND USE OF ANTI-INTEGRIN ANTIBODIES FOR THE
; TITLE OF INVENTION: CONTROL OF TISSUE GRANULATION
; FILE REFERENCE: 05882.0186.NPUS01
; CURRENT APPLICATION NUMBER: US/10/818,068
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-818-068-9

Query Match 80.8%; Score 42; DB 16; Length 109;
Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9
DB 90 HOYLRSPYT 98

RESULT 5
US-10-818-068-10
; Sequence 10, Application US/10818068
; Publication No. US20050002930A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: METHODS OF PRODUCTION AND USE OF ANTI-INTEGRIN ANTIBODIES FOR THE
; TITLE OF INVENTION: CONTROL OF TISSUE GRANULATION
; FILE REFERENCE: 05882.0186.NPUS01
US-10-818-068-10

ALIGNMENTS

RESULT 1
S61665
probable membrane protein YOR107w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein O3224; hypothetical protein YOR3224w
C/Species: Saccharomyces cerevisiae
C/Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C/Accession: S61665; S66992
R/Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banreyl, A.; Sander, C.; Valencia
submitted to the EMBL Data Library, December 1995
A/Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome
A/Reference number: S61643
A/Accession: S61665
A/Molecule type: DNA
A/Residues: 1-309 <BEN>
A/Cross-references: UNIPROT:Q99188; EMBL:X94335; NID:g1262139; PID:e217829; PID:g1164952
R/Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansoerge, W.
submitted to the Protein Sequence Database, July 1996
A/Reference number: S66965
A/Accession: S66992
A/Molecule type: DNA
A/Residues: 1-309 <VOS>
A/Cross-references: EMBL:Z75015; NID:g1420290; PID:e252009; PID:g1420291; MIPS:YOR107w
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:RGS2
A/Cross-references: SGD:S0005633
A/Map position: 15R
C/Superfamily: Saccharomyces cerevisiae probable membrane protein YOR107w
C/Keywords: transmembrane protein
F:129-145/Domain: transmembrane #status predicted <TMM>
Query Match 73.1%; Score 38; DB 2; Length 309;
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 HOYLRSPYT 9
|:|:|:|:|
Db 39 HERMRSPYT 47
|:|:|:|:|
RESULT 2
PH1059
Ig light chain V region (clone 17s-cl) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: PH1059
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH1059
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-99 <TIL>
A/Experimental source: B cell, strain [NZB x NZW]F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>
Query Match 71.2%; Score 37; DB 2; Length 99;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 HOYLRSPYT 9
|:|:|:|:|
Db 90 HOYHRSPYT 98
|:|:|:|:|
RESULT 3
S46373

Ig kappa chain V-J region (T24-9) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C/Accession: S46373; S38647
R/Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chI) gene rear
A/Reference number: S46369; MUID:94313975; PMID:8039491
A/Accession: S46373
A/Molecule type: mRNA
A/Residues: 1-132 <BEN>
A/Cross-references: EMBL:Z27174; NID:g415963; PIDN:CA481698.1; PID:g415964
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:34-114/Domain: immunoglobulin homology <IMM>
Query Match 71.2%; Score 37; DB 2; Length 132;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HOYLRSPYT 9
|:|:|:|:|
Db 113 HOYSSPFT 121
|:|:|:|:|

RESULT 4
D71460
probable membrane thiol proteinase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C/Species: Chlamydia trachomatis
C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C/Accession: D71460
R/Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marache, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tract
A/Reference number: A71570; MUID:9900809; PMID:9784136
A/Accession: D71460
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-418 <ARN>
A/Cross-references: UNIPROT:O84876; GB:AE001360; GB:AE001273; NID:g3329342; PIDN:AA68466
A/Experimental source: serotype D, strain UW-3/Cx
C/Genetics:
A/Gene: CT868
Query Match 71.2%; Score 37; DB 2; Length 418;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HOYLRSPYT 9
|:|:|:|:|
Db 367 HWYLRDPFT 375
|:|:|:|:|

RESULT 5
JQ1744
hypothetical 77.2K protein - rabbit fibroma virus
N/Alternate names: H3r protein
C/Species: rabbit fibroma virus, Shope fibroma virus
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JQ1744
R/Masung, R.F.; McFadden, G.; Moyer, R.W.
J. Gen. Virol. 73, 2903-2911, 1992
A/Title: Nucleotide sequence analysis of a unique near-terminal region of the tumorigenic
A/Reference number: JQ1741; MUID:93057362; PMID:1331293
A/Accession: JQ1744
A/Molecule type: DNA
A/Residues: 1-673 <MAS>
A/Cross-references: UNIPROT:Q9G8T5
Query Match 71.2%; Score 37; DB 2; Length 673;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 24, 2005, 08:54:17 ; Search time 59.3438 Seconds
(without alignments)
77.661 Million cell updates/sec

Title: US-10-018-245A-6
Perfect score: 52
Sequence: 1 HQYLRSPYT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	82.7	170	2	O8N2E2
2	43	82.7	565	2	O7MEIO
3	42	80.8	333	2	O6NXYO
4	42	80.8	447	1	CRDL_MOUSE
5	42	80.8	521	2	O7ELDO
6	41	78.8	234	1	NPD_IACPL
7	39	75.0	909	2	O7JPB1
8	39	75.0	911	2	O7JPB0
9	38	73.1	88	2	O49251
10	38	73.1	197	2	O9Z499
11	38	73.1	289	2	O7VGV4
12	38	73.1	309	2	O99188
13	38	73.1	336	1	RT09_CANAL
14	38	73.1	403	2	O9RUT8
15	38	73.1	496	2	O81UF7
16	38	73.1	760	2	O8BXL8
17	37	71.2	168	2	O691W6
18	37	71.2	418	2	O84876
19	37	71.2	446	2	O6AUF8
20	37	71.2	488	2	O91GHI
21	37	71.2	588	2	O82G94
22	37	71.2	626	2	O8RUK0
23	37	71.2	635	2	O6CDF3
24	37	71.2	639	2	O6CH21
25	37	71.2	639	2	O6C1X7
26	37	71.2	673	2	O9Q8T5
27	37	71.2	675	2	O9Q8R6
28	37	71.2	916	2	O6K1V9
29	37	71.2	1089	2	O6C3L8
30	37	71.2	1111	1	SEC8_NEUCR
31	37	71.2	1171	2	O7YXU7

32	37	71.2	1794	2	O9S168	O9e168 arabidopsis
33	36.5	70.2	388	2	O54142	O54142 streptomyc
34	36	69.2	322	2	O17066	O17066 caenorhabd
35	36	69.2	363	2	O07544	O07544 bacillus su
36	36	69.2	480	2	O2HB39	O2hb39 homo sapien
37	36	69.2	484	1	Y330_SHEON	O6ejx6 shewanella
38	36	69.2	514	2	O8GW03	O8gw03 oryza sativ
39	36	69.2	534	2	O9HB38	O9hb38 homo sapien
40	36	69.2	548	2	O8MWQ1	O8mwq1 homo sapien
41	36	69.2	592	2	O8MWQ2	O8mwq2 homo sapien
42	36	69.2	592	2	O2HB37	O2hb37 homo sapien
43	36	69.2	693	2	O8GVZ1	O8gvz1 oryza sativ
44	36	69.2	778	2	O8U8F7	O8u8f7 agrobacteri
45	36	69.2	916	2	O8RXJ5	O8rxj5 arabidopsis
46	36	69.2	931	2	O04026	O04026 arabidopsis
47	36	69.2	936	2	O04025	O04025 arabidopsis
48	35	67.3	89	2	O48636	O48636 alstroemer
49	35	67.3	91	2	O9N3P7	O9np37 caenorhabd
50	35	67.3	165	2	O6K652	O6k652 oryza sativ
51	35	67.3	246	2	O818T7	O818t7 arabidopsis
52	35	67.3	251	2	O9FMW9	O9fmm9 arabidopsis
53	35	67.3	345	2	O56F06	O56f06 vibrio chol
54	35	67.3	486	1	THRC_HELPJ	O9zmx5 helicobacte
55	35	67.3	486	1	THRC_HELPY	O24924 helicobacte
56	35	67.3	538	2	O86030	O86030 vibrio chol
57	35	67.3	598	2	O8B0U3	O8b0u3 helicobasid
58	35	67.3	609	2	O8A532	O8a532 bacteroides
59	35	67.3	641	2	O52824	O52824 rhizobium l
60	35	67.3	641	2	O9FDG2	O9fdg2 rhizobium e
61	35	67.3	663	1	SEPI_SCHPO	O43058 schizosacch
62	35	67.3	705	2	O87192	O87192 vibrio para
63	35	67.3	718	2	O7ROI1	O7rgi1 plasmodium
64	35	67.3	818	1	COLA_VIBCH	O9crj0 vibrio chol
65	35	67.3	899	2	O96237	O96237 plasmodium
66	35	67.3	906	2	O7REWS	O7rbws plasmodium
67	35	67.3	1040	2	O7OG14	O7og14 amophiles g
68	35	67.3	1358	2	O6Q474	O6q474 porphyromon
69	35	67.3	1732	2	O07442	O07442 porphyromon
70	35	67.3	1732	2	O52050	O52050 porphyromon
71	35	67.3	1732	2	O51817	O51817 porphyromon
72	35	67.3	1732	2	O9N533	O9n533 caenorhabd
73	35	67.3	3901	2	O49240	O49240 alstroemer
74	34	65.4	89	2	O7WLR5	O7wlr5 bordetella
75	34	65.4	136	2	O8HP94	O8hp94 ciindela r
76	34	65.4	136	2	O8HPB7	O8hpb7 ciindela c
77	34	65.4	140	2	O94TP6	O94tp6 ciindela c
78	34	65.4	143	2	O8HP95	O8hp95 ciindela m
79	34	65.4	159	2	O8HP81	O8hp81 ciindela b
80	34	65.4	161	2	O94TP4	O94tp4 ciindela m
81	34	65.4	162	2	O94TK3	O94tk3 pentacomia
82	34	65.4	162	2	O94TK5	O94tk5 ciindela u
83	34	65.4	162	2	O94TK7	O94tk7 ciindela c
84	34	65.4	162	2	O94TL1	O94tl1 ciindela d
85	34	65.4	162	2	O94TL4	O94tl4 ciindela p
86	34	65.4	162	2	O94TP5	O94tp5 ciindela b
87	34	65.4	162	2	O94TP7	O94tp7 ciindela a
88	34	65.4	162	2	O94TP8	O94tp8 ciindela t
89	34	65.4	162	2	O94TP9	O94tp9 ciindela l
90	34	65.4	162	2	O94TQ0	O94tq0 ciindela d
91	34	65.4	162	2	O94TQ1	O94tq1 ciindela o
92	34	65.4	162	2	O94TQ2	O94tq2 ciindela c
93	34	65.4	162	2	O8HP75	O8hp75 ciindela n
94	34	65.4	162	2	O8HP75	O8hp75 ciindela c
95	34	65.4	162	2	O8HP89	O8hp89 ciindela c
96	34	65.4	162	2	O8HP90	O8hp90 ciindela v
97	34	65.4	162	2	O8HP96	O8hp96 ciindela t
98	34	65.4	162	2	O8HP97	O8hp97 ciindela r
99	34	65.4	162	2	O8HPA2	O8hpa2 ciindela s
100	34	65.4	162	2	O8HPB0	O8hpb0 ciindela o

ALIGNMENTS

```
RESULT 1
Q8N2E2 PRELIMINARY; PRT; 170 AA.
ID Q8N2E2
AC Q8N2E2;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE Hypothetical protein PSEC0224.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RA Oca T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Makamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
SQ EMBL; AK075525; BAC1671.1;
DR SEQUENCE 170 AA; 18999 MW; 38EP957175E50D73 CRC64;

Query Match      82.7%; Score 43; DB 2; Length 170;
Best Local Similarity 87.5%; Pred. No. 2.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLRSPPY 8
Db 28 HQFLRSPY 35

RESULT 2
Q7MEIO PRELIMINARY; PRT; 565 AA.
ID Q7MEIO
AC Q7MEIO;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Hypothetical protein VVA0690.
OS OrderedLocustNames=VVA0690;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_Taxid=196600;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14655965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-Y., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
DR EMBL; AP005347; BAC96716.1;
DR InterPro; IPR002789; DUF87.
DR Pfam; PF01935; DUF87.1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 565 AA; 62426 MW; 478F1601A7F1E98E CRC64;

Query Match      82.7%; Score 43; DB 2; Length 565;
Best Local Similarity 87.5%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLRSPPY 8
Db 440 HQYLRDPY 447

RESULT 3
Q6NXYO PRELIMINARY; PRT; 333 AA.
ID Q6NXYO
AC Q6NXYO;
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DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Chrd11 protein.
GN Chrd11
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD1; TISSUE=Neural Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA DiChien L., Marins A.K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CD1; TISSUE=Neural Stem Cell;
RX Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC066832; AAH66832.1;
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR01007; VWF_C.
DR Pfam; PF00093; VMC_3.
DR SMART; SM00214; VMC_3.
DR PROSITE; PS01208; VWF_C_1; 3.
DR PROSITE; PS50184; VWF_C_2; 3.
SQ SEQUENCE 333 AA; 37035 MW; A82093A24174E1D6 CRC64;

Query Match      80.8%; Score 42; DB 2; Length 333;
Best Local Similarity 87.5%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLRSPPY 8
Db 199 HSYLRSPY 206

RESULT 4
CRDL_MOUSE STANDARD; PRT; 447 AA.
ID CRDL_MOUSE
AC Q920G1; O924KO; Q9EP29;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chordrin-like protein 1 precursor (Neuratin) (Ventropilin).
GN Name=Chrd11; Synonyms=Wrln1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC STRAIN=C57BL/6J;
RX MEDLINE=21334726; PubMed=11441185; DOI=10.1126/science.1058379;
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